

36/985

Title: Modulating developmental pathways in plants.

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The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The different domains of RKS gene products essentially have the following functions: The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane domain. At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062, WO 01/29240). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

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Plant homologs of the Arabidopsis RKS genes can be found by comparison of various plant database (see also Table 2) and comprise amongst others:

- 5    Y14600|SBRLK1|*Sorghum bicolor*  
BF004020|BF004020|EST432518 KV1 *Medicago truncatata*  
AW934655|AW934655|EST353547 tomato  
AW617954|AW617954|EST314028 *L. pennellii*  
AA738544|AA738544|SbRLK2 *Sorghum bicolor*
- 10   AA738545|AA738545|SbRLK3 *Sorghum bicolor*  
BG595415|BG595415|EST494093 cSTS *Solanum tuberosa*  
AI896277|AI896277|EST265720 tomato  
BF643238|BF643238|NF002H05EC1F1045  
AA738546|AA738546|SbRLK4 *Sorghum bicolor*
- 15   BE658174|BE658174|GM700005A20D5 Gm-r1070 *Glycine max*  
BF520845|BF520845|EST458318 DSIL *Medicago truncata*  
AC069324|AC069324|*Oryza sativa*  
AW761055|AW761055|sl70d06.y1 Gm-cl027 *Glycine max*  
BE352622|BE352622|WHE0425\_G11\_M21ZS Wheat
- 20   BG647340|BG647340|EST508959 HOGA *Medicago truncata*  
AY028699|AY028699|*Brassica napus*  
AW666082|AW666082|sk31h04.y1 Gm-cl028 *Glycine max*  
AA738547|AA738547|SbRLK5 *Sorghum bicolor*  
BG127658|BG127658|EST473220 tomato
- 25   L27821|RICPRKI|*Oryza sativa*  
BG238468|BG238468|sab51a09.y1 Gm-cl043 *Glycine max*  
BG441204|BG441204|GA\_Ea0012C15f *Gossypium arbo.*  
AW667985|AW667985|GA\_Ea0012C15 *Gossypium arbore.*  
AW233982|AW233982|sf32g05.y1 Gm-cl028 *Glycine max*
- 30   AP003235|AP003235|*Oryza sativa*  
BF460294|BF460294|074A05 Mature tuber  
AY007545|AY007545|*Brassica napus*  
AC087544|AC087544|*Oryza sativa*  
AB041503|AB041503|*Populus nigra*

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The invention furthermore relates to modifying ELS genes or gene products or functional equivalents thereof which are for example derived from at least two different genes in the

40   Arabidopsis genome. They show high homology on protein level

with the corresponding transmembrane RKS gene products.  
 However, they lack a transmembrane domain while they do  
 contain a signaling sequence at the N-terminal end. Therefore  
 these proteins are thought to be positioned within vesicles  
 5 within the plant cell or at the outside of the plasma  
 membrane, within the cell wall of the plant cell. A number of  
 homologs have been detected in other plant species, such as:

- AF370543|AF370543|*Arabidopsis thaliana*  
 10 AF324989|AF324989|*Arabidopsis thaliana*  
AV520367|AV520367|*Arabidopsis thaliana*  
AV553051|AV553051|*Arabidopsis thaliana*  
BF642233|BF642233|NF050C09IN1F1069  
AW559436|AW559436|EST314484 *DSIR Medicago truncata*  
 15 BG456991|BG456991|NF099F02PL1F1025  
AW622146|AW622146|EST312944 tomato  
BF260895|BF260895|HVSMEf0023D15f *Hordeum vulgare*  
BE322325|BE322325|NF022E12IN1F1088  
BG414774|BG414774|HVSMEk0003K21f *Hordeum vulgare*  
 20 BE460627|BE460627|EST412046 tomato  
BI204894|BI204894|EST522934 *ctOS Lycopersicon esculentum*  
BI205306|BI205306|EST523346 *ctOS Lycopersicon esculentum*  
BI204366|BI204366|EST522406 *ctOS Lycopersicon esculentum*  
AW443205|AW443205|EST308135 tomato  
 25 AW031110|AW031110|EST274417 tomato  
BI180080|BI180080|EST521025 *cSTE Solanum tuberosa*  
BF644761|BF644761|NF015A11EC1F1084  
AV526127|AV526127|*Arabidopsis thaliana*  
AV556193|AV556193|*Arabidopsis thaliana*  
 30 BE203316|BE203316|EST403338 *KV1 Medicago truncatata*.  
AW649615|AW649615|EST328069 tomato  
BE512465|BE512465|946071E06  
BI204917|BI204917|EST522957 *ctOS Lycopersicon esculentum*  
BG590749|BG590749|EST498591  
 35 BG648725|BG648725|EST510344 *HOGA Medicago truncata*  
BG648619|BG648619|EST510238 *HOGA Medicago truncata*  
BG597757|BG597757|EST496435 *cSTS Solanum tuberosa*  
AW221939|AW221939|EST298750 tomato  
BE704836|BE704836|Sc01\_  
 40 BG124409|BG124409|EST470055 tomato

- BF051954 | BF051954 | EST437120 tomato  
BG320355 | BG320355 | Zm03\_05h01\_Zea mays  
AV526624 | AV526624 | Arabidopsis thaliana  
AW933960 | AW933960 | EST359803 tomato
- 5 AW221278 | AW221278 | EST297747 tomato  
BE405514 | BE405514 | WHE1212\_C01\_F02ZS Wheat  
BG314461 | BG314461 | WHE2495\_A12\_A23ZS *Triticum*  
BF258673 | BF258673 | HVSMEf0016G01f *Hordeum vulgare*  
BG262637 | BG262637 | WHE0938\_E03\_I06ZS Wheat
- 10 AW030188 | AW030188 | EST273443 tomato  
BG653580 | BG653580 | sad76b11.y1 Gm-cl051 *Glycine max*  
BG319729 | BG319729 | Zm03\_05h01\_A Zm03\_Zea mays  
BF053590 | BF053590 | EST438820 potato  
BE454808 | BE454808 | HVSMEh0095C03f *Hordeum vulgare*
- 15 BI075801 | BI075801 | IP1\_21\_D05.b1\_A002  
BE367593 | BE367593 | PI1\_9\_F02.b1\_A002 *Sorghum bicolor*  
2e-074 BF260080 | BF260080 | HVSMEf0021A22f *Hordeum vulgare*  
BF627921 | BF627921 | HVSMEb0006I23f *Hordeum vulgare*  
BG598491 | BG598491 | EST503391 cSTS *Solanum tuberosa*
- 20 AW038168 | AW038168 | EST279825 tomato  
BG343258 | BG343258 | HVSMEg0005D23f *Hordeum vulgare*  
AW925684 | AW925684 | HVSMEg0005D23 *Hordeum vulgare*  
BG416093 | BG416093 | HVSMEk0009L18f *Hordeum vulgare*  
AW683370 | AW683370 | NF011C09LF1F1069
- 25 BE420108 | BE420108 | WWS020.C1R000101 ITEC WWS Wheat  
AW350720 | AW350720 | GM210009A10F4 Gm-r1021 *Glycine max*  
AW616564 | AW616564 | EST322975 *L. Hirsutum trichome*  
AW011134 | AW011134 | ST17B03 Pine  
BF630746 | BF630746 | HVSMEb0013N06f *Hordeum vulgare*
- 30 AW926045 | AW926045 | HVSMEg0006C10 *Hordeum vulgare*  
BE519800 | BE519800 | HV\_CEb0021E12f *Hordeum vulgare*  
BG343657 | BG343657 | HVSMEg0006C10f *Hordeum vulgare*  
BG933682 | BG933682 | OV1\_16\_C09.b1\_A002  
BE433368 | BE433368 | EST399897 tomato
- 35 AW219797 | AW219797 | EST302279 tomato  
BF629324 | BF629324 | HVSMEb0010N06f *Hordeum vulgare*  
BE597128 | BE597128 | PI1\_71\_A07.g1\_A002  
AW220075 | AW220075 | EST302558 tomato  
AW616639 | AW616639 | EST323050 *L. Hirsutum trichome*
- 40 BF645214 | BF645214 | NF032F11EC1F1094  
AW924540 | AW924540 | WS1\_70\_H12.b1\_A002

- AI775448|AI775448|EST256548 tomato  
AW983360|AW983360|HVSMEg0010F15f *Hordeum vulgare*  
BF270171|BF270171|GA\_Eb0007B13f *Gossypium arbor.*  
BE919631|BE919631|EST423400 potato
- 5 AW037836|AW037836|EST279465 tomato  
BF008781|BF008781|ss79h09.y1 Gm-cl064 *Glycine max*  
BF254651|BF254651|HVSMEf0004K05f *Hordeum vulgare*  
BE599797|BE599797|PI1\_79\_H01.g1\_A002  
BE599026|BE599026|PI1\_86\_E03.g1\_A002
- 10 R89998|R89998|16353 Lambda-PRL2 *Arabidopsis*  
BG841108|BG841108|MEST15-G02.T3 ISUM4-TN *Zea mays*  
AW307218|AW307218|sf54c07.y1 Gm-cl009 *Glycine max*  
AI496325|AI496325|sb05c09.y1 Gm-cl004 *Glycine max*  
AJ277703|ZMA277703|*Zea mays*
- 15 AL375586|CNS0616P|*Medicago truncatula* EST  
AW350549|AW350549|GM210009A10A12 Gm-r1021 *Glycine max*  
BE125918|BE125918|DG1\_59\_F02.b1\_A002  
BF053901|BF053901|EST439131 potato  
BE921389|BE921389|EST425266 potato
- 20 BE597551|BE597551|PI1\_71\_A07.b1\_  
BE360092|BE360092|DG1\_61\_C09.b1\_A002  
BE660084|BE660084|491 GmaxSC *Glycine max*  
AJ277702|ZMA277702|*Zea mays*
- 25 The invention also relates to modifying SBP/SPL gene or  
 products which represent a family of transcription factors  
 with a bipartite nuclear localization signal (The SQUAMOSA  
 PROMOTER-BINDING PROTEIN-LIKE (SBP/SPL) gene family of  
*Arabidopsis thaliana*, Columbia ecotype). Upon activation
- 30 (probably by RKS mediated phosphorylation, the bipartite  
 nuclear localization signal becomes linear and available for  
 the nuclear translocation of the protein. Within the plant  
 nucleus, the transcription factor regulates transcription by  
 interaction with specific promoter elements. .In *Arabidopsis*
- 35 *thaliana*, this family is represented by at least 16 different  
 members (see following list). In many other plant species, we  
 also identified members of this transcription factor family  
 (See list on page 7).

Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation: <http://www.ub.uni-koeln.de/ediss/archiv/2001/11wl204.pdf>; Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

20

	name	genetic code
	ATSPL1	At2g47070*
	ATSPL2	At5g43270
	ATSPL3	At2g33810*
25	ATSPL4	At1g53160*
	ATSPL5	At3g15270
	ATSPL6	At1g69170
	ATSPL7	At5g18830
	ATSPL8	At1g02065
30	ATSPL9	At2g42200*
	ATSPL10	At1g27370*
	ATSPL11	At1g27360*
	ATSPL12	At3g60030
	ATSPL13	At5g50570
35	ATSPL14	At1g20980
	ATSPL15	At3g57920
	ATSPL16	At1g76580

\* annotation in database not complete and/or correct

In many other plant species, we identified members of this transcription factor family, plant homologs of the Arabidopsis SBP/SPL proteins are for example:

- 5    AB023037|AB023037|*Arabidopsis thaliana*  
BG789832|BG789832|sae56b07.y1 *Gm-c1051 Glycine max*  
BG123992|BG123992|EST469638 *tomato*  
BG595750|BG595750|EST494428 *cSTS Solanum tuberosum*  
AF370612|AF370612|*Arabidopsis thaliana*
- 10   BF728335|BF728335|1000060H02.x1 1000 - *Zea mays*  
X92079|AMSBP2|*A.majus*  
AW331087|AW331087|707047A12.x1 707 - Mixed adult... 128 zea mays  
AJ011643|ATH011643|*Arabidopsis thaliana*  
L34039|RICRMSOA|*Oryza sativa*
- 15   AJ011638|ATH011638|*Arabidopsis thaliana*  
AJ011639|ATH011639|*Arabidopsis thaliana*  
AJ132096|ATH132096|*Arabidopsis thaliana*  
BF482644|BF482644|WHE2301-2304\_A21\_A21ZS *Wheat*  
BF202242|BF202242|WHE0984\_D01\_G02ZS *Wheat*
- 20   BE057470|BE057470|sm58e10.y1 *Gm-c1028 Glycine max*  
AJ011628|ATH011628|*Arabidopsis thaliana*  
AJ011629|ATH011629|*Arabidopsis thaliana*  
AJ011617|ZMA011617|*Zea mays*  
AJ011637|ATH011637|*Arabidopsis thaliana*
- 25   AJ011622|AMA011622|*Antirrhinum majus*  
AJ011621|AMA011621|*Antirrhinum majus*  
AJ011635|ATH011635|*Arabidopsis thaliana*  
AJ011623|AMA011623|*Antirrhinum majus*  
BF650908|BF650908|NF098D09EC1F1076
- 30   AJ242959|ATH242959|*Arabidopsis thaliana*  
Y09427|ATSPL3|*A.thaliana* mRNA  
AJ011633|ATH011633|*Arabidopsis thaliana*  
AW691786|AW691786|NF044B06ST1F1000  
BE058432|BE058432|sn16a06.y1 *Gm-c1016 Glycine max*
- 35   AW728623|AW728623|GA\_Ea0017G06 *Gossypium arbore.*  
BG442540|BG442540|GA\_Ea0017G06f *Gossypium arbo.*  
AJ011626|ATH011626|*Arabidopsis thaliana*  
AJ011625|ATH011625|*Arabidopsis thaliana*  
AI993858|AI993858|701515182 *A. thaliana*
- 40   BG593787|BG593787|EST492465 *cSTS Solanum tuberosum*  
BF634536|BF634536|NF060C08DT1F1065 *Drought Medicago*

- BE806499|BE806499|ss59f10.y1 Gm-cl062 *Glycine max*  
AW933950|AW933950|EST359793 tomato  
AC008262|AC008262| *Arabidopsis*  
B28493|B28493|T10A24TF TAMU *Arabidopsis thaliana*  
5 AJ011644|ATH011644|*Arabidopsis thaliana*  
AC018364|AC018364|*Arabidopsis thaliana*  
AL092429|CNS00VLB|*Arabidopsis thaliana*  
BE435668|BE435668|EST406746 tomato  
BG097153|BG097153|EST461672 potato  
10 BE440574|BE440574|sp47b09.y1 Gm-cl043 *Glycine max*  
AI443033|AI443033|sa31a08.y1 Gm-cl004 *Glycine max*  
U89496|ZMU89496|*Zea mays liguleless1*  
AW433271|AW433271|sh54g07.y1 Gm-cl015 *Glycine max*  
AW932595|AW932595|EST358438 tomato  
15 AW096676|AW096676|EST289856 tomato  
AJ011616|ZMA011616|*Zea mays*  
AW036750|AW036750|EST252139 tomato  
BF626329|BF626329|HVSMEa0018F24f *Hordeum vulgare*  
AJ011614|ZMA011614|*Zea mays*  
20 AJ011642|ATH011642|*Arabidopsis thaliana*  
BE022435|BE022435|sm85h04.y1 Gm-cl015 *Glycine max*  
X92369|AMSPB1|*A.majus*  
AC015450|AC015450|*Arabidopsis thaliana*  
AC079692|AC079692|*Arabidopsis thaliana*  
25 AJ011632|ATH011632|*Arabidopsis thaliana*  
AJ011631|ATH011631|*Arabidopsis thaliana*  
BE455349|BE455349|HVSMEh0097E20f *Hordeum vulgare*  
AJ242960|ATH242960|*Arabidopsis thaliana*  
AJ011610|ATH011610|*Arabidopsis thaliana*  
30 AJ132097|ATH132097|*Arabidopsis thaliana*  
AL138658|ATT209|*Arabidopsis thaliana*  
AJ011615|ZMA011615|*Zea mays*  
BE499739|BE499739|WHE0975\_ Wheat  
AW398794|AW398794|EST309294 *L. pennellii*  
35 AJ011618|ZMA011618|*Zea mays*  
AW747167|AW747167|WS1\_66\_F11.b1\_  
AJ011577|ATH011577|*Arabidopsis thaliana*  
AI992727|AI992727|701493410 *A. thaliana*  
BE060783|BE060783|HVSMEg0013F15f *Hordeum vulgare*  
40 BE804992|BE804992|ss34h10.y1 Gm-cl061 *Glycine max*  
BE325341|BE325341|NF120H09ST1F1009

- AC007369|AC007369|*Arabidopsis thaliana*  
AJ011619|ZMA011619|*Zea mays*  
BI099345|BI099345|IP1\_37\_H10.b1\_A002  
BI071295|BI071295|C054P79U *Populus*  
5 AZ920400|AZ920400|1006019G01.y2 1006 -  
AZ919034|AZ919034|1006013G02.x3 1006 -  
BE805023|BE805023|ss35d09.y1 Gm-cl061 *Glycine max*  
BG582086|BG582086|EST483824 GVN *Medicago truncata*  
AJ011609|ATH011609|*Arabidopsis thaliana*  
10 BE023083|BE023083|sm90e08.y1 Gm-cl015 *Glycine max*

- Furthermore, the invention relates to modifying NDR-NHL-genes  
or gene products. All proteins belonging to this family  
contain one (and sometimes even more than one) transmembrane  
15 domain. *Arabidopsis* contains a large number of NDR-NHL genes,  
such as:  
aad21459, aaf18257, aac36175, k10d20 (position 40852-41619),  
aad21460, cab78082, aad21461, aad42003, aaf02134, aaf187656,  
aaf02133, cab43430, cab88990, cab80950, aad25632, aaf23842, all63812,  
20 f20d21-35, t13m11-12, fle22-7, t23g18, f5d14-4266, t32f12-16, f11f19-  
11, f11f19-12, f11f19-13, t20p8-13, f12k2, f23h14, k10d20-44043,  
k10d20-12, t19f11-6, t19f11-5, t10d17-10, f22o6-150, f3d13-5, m3e9-  
80, t25p22-30, mhf15-4, mhf15-5, mrn17-4, mlf18-9, mgn6-11994, mjj3-  
9667, f14f18-60, At1g17620 F11A6, At5g11890 , At2g27080 , At5g36970 ,  
25 mlf18 , At1g65690 F1E22 , At4g01110 F2N1 , At2g35980 f11f19 ,  
At4g01410 F3D13 , At1g54540 F20D21 , At2g46300 t3f17 , At5g21130 ,  
At3g11650 T19F11 , At5g06320 MHF15 , At5g06330 MHF15 , At2g01080  
f15b18 , At2g35460 t32f12 , At2g27260 f12k2 , At2g35970 f11f19 ,  
At5g53730 MGN6 , At5g22870 MRN17 , At4g09590 , At3g54200 , At1g08160  
30 T6D22 , At5g22200 , At3g52470 , At2g35960 f11f19 , At3g52460 ,  
At5g56050 MDA7, At3g20590 K10D20 , At1g61760 T13M11 , At3g20600  
K10D20 , At1g13050 F3F19 , At3g11660 T19F11 , At3g44220 , At1g64450  
F1N19 , At3g26350 F20C19 C , At4g05220 , At5g45320 K9E15 ,  
At4g23930 , At4g13270 , At4g39740 , At1g45688 F2G19 W , At5g42860  
35 MBD2 , At1g32270 F27G20 , At4g30660 , At2g45430 f4l23 , At4g30650 ,  
At1g69500 F10D13

and

- 40 ndr1, At2g27080; T20P8.13, At5g21130, At1g65690, At5g36970,

- At1g54540, At5g06320, At5g11890, At1g17620, At3g11650, At2g22180,  
 At5g22870, At2g35980, At2g46300, At4g05220, At2g35460, At2g27260,  
 At4g01410, At5g22200, At1g61760, At3g52470, At5g53730, At4g01110,  
 At2g35960, At3g52460, At4g09590, At2g35970, At3g26350, At3g11660,  
 5 At3g44220, At1g08160, At2g01080, At5g06330, At5g56050, At3g20600,  
 NDR1, At3g54200, At3g20590, At4g39740, At1g32270 syntaxin, putative,  
 At1g13050, At5g45320, At3g20610, At4g26490, At5g42860, At1g45688,  
 At4g26820
- 10 NDR-NHL genes belong to a large family of which one of the  
 first identified is the defence-associated gene HIN1 (Harpin-  
 induced gene). HIN1 is transcriptionally induced by harpins  
 and bacteria, that elicit hypersensitive responses in tobacco.  
 It is thus believed that the genes of the invention also play  
 15 arole in the hypersensitive reaction. Especially (see also  
 chapter 8) since the genes of the invention bear relation to  
 brassinoid-like responses and since brassinoid pathway  
 compounds have been found to interact in this same defence  
 system in plants. Other plant species also contain members of  
 20 this large gene family, such as:

Plant homologs of the *Arabidopsis* NDR/NHL genes:

- 25 BG582276|BG582276|EST484016 GVN *Medicago truncata*  
AV553539|AV553539|*Arabidopsis thaliana*  
AC069325|AC069325|*Arabidopsis thaliana*  
AV526693|AV526693|*Arabidopsis thaliana*  
BG583456|BG583456|EST485208 GVN *Medicago truncata*  
 30 AW267833|AW267833|EST305961 DSIR *Medicago truncata*  
BE997791|BE997791|EST429514 GVSN *Medicago truncata*  
BG580928|BG580928|EST482657 GVN *Medicago truncata*  
BF520916|BF520916|EST458389 DSIL *Medicago truncata*  
AV544651|AV544651|*Arabidopsis thaliana*  
 35 AV543762|AV543762|*Arabidopsis thaliana*  
AW559665|AW559665|EST314777 DSIR *Medicago truncata*  
BG581012|BG581012|EST482741 GVN *Medicago truncata*  
AV552164|AV552164|*Arabidopsis thaliana*  
BE999881|BE999881|EST431604 GVSN *Medicago truncata*  
 40 AW031098|AW031098|EST274405 tomato

- AI998763|AI998763|701546833 *A. thaliana*  
AW219286|AW219286|EST301768 tomato  
BE124562|BE124562|EST393597 *GVN Medicago truncata*  
AV540371|AV540371|*Arabidopsis thaliana*  
5 AV539549|AV539549|*Arabidopsis thaliana*  
BG647432|BG647432|EST509051 *HOGA Medicago truncata*  
BE434210|BE434210|EST405288 tomato  
BG725849|BG725849|sae42g02.y1 *Gm-cl051 Glycine max*  
AP003247|AP003247|*Oryza sativa*  
10 BE348073|BE348073|spl1a11.y1 *Gm-cl042 Glycine max*  
AW508383|AW508383|si40c06.y1 *Gm-r1030 Glycine max*  
AI856504|AI856504|sb40b07.y1 *Gm-cl014 Glycine max*  
BE556317|BE556317|sq01b07.y1 *Gm-cl045 Glycine max*  
AA713120|AA713120|32681 *Arabidopsis*  
15 AV541531|AV541531|*Arabidopsis thaliana*  
AI894456|AI894456|EST263911 tomato  
AW704493|AW704493|sk53g11.y1 *Gm-cl019 Glycine max*  
AW219298|AW219298|EST301780 tomato  
BF425685|BF425685|ss03c11.y1 *Gm-cl047 Glycine max*  
20 AV422557|AV422557|*Lotus japonicus*  
BE190816|BE190816|sn79a08.y1 *Gm-cl038 Glycine max*  
BG580331|BG580331|EST482056 *GVN Medicago truncata*  
AV423251|AV423251|*Lotus japonicus*  
AI896088|AI896088|EST265531 tomato  
25 AV413427|AV413427|*Lotus japonicus*  
AV426656|AV426656|*Lotus japonicus*  
AV416256|AV416256|*Lotus japonicus*  
AL385732|CNS0690I|*Medicago truncatula*  
AB016877|AB016877|*Arabidopsis thaliana*  
30 AV419449|AV419449|*Lotus japonicus*  
AI486269|AI486269|EST244590 tomato  
AV411690|AV411690|*Lotus japonicus*  
AV419925|AV419925|*Lotus japonicus*  
AV418222|AV418222|*Lotus japonicus*  
35 AV409427|AV409427|*Lotus japonicus*  
AC005287|AC005287|*Arabidopsis thaliana*  
AV426716|AV426716|*Lotus japonicus*  
AV411791|AV411791|*Lotus japonicus*  
BG351730|BG351730|131E12 Mature tuber  
40 BG046452|BG046452|saa54b12.y1 *Gm-cl060 Glycine max*  
AI781777|AI781777|EST262656 tomato

- BE451428|BE451428|EST402316 tomato  
AI772944|AI772944|EST254044 tomato  
AI895510|AI895510|EST264953 tomato  
AW030762|AW030762|EST274017 tomato  
5 AW218859|AW218859|EST301341 tomato  
BE203936|BE203936|EST396612 KVO *Medicago truncata*  
AV410289|AV410289|*Lotus japonicus*  
AW032019|AW032019|EST275473 tomato  
AW030868|AW030868|EST274158 tomato  
10 AV421824|AV421824|*Lotus japonicus*  
BG646408|BG646408|EST508027 HOGA *Medicago truncata*  
AF325013|AF325013|*Arabidopsis thaliana*  
AC007234|AC007234|*Arabidopsis thaliana*  
AW217237|AW217237|EST295951 tomato  
15 AC034257|AC034257|*Arabidopsis thaliana*  
AW625608|AW625608|EST319515 tomato  
AW031064|AW031064|EST274371 tomato  
AF370332|AF370332|*Arabidopsis thaliana*  
AB006700|AB006700|*Arabidopsis thaliana*  
20 AW035467|AW035467|EST281205 tomato  
AL163812|ATF14F18|*Arabidopsis thaliana*  
AI896652|AI896652|EST266095 tomato  
AI730803|AI730803|BNLGHi7970 Cotton  
AW034775|AW034775|EST278811 tomato

25

- The invention provides the insight that RKS proteins or functional equivalents thereof play part in a signaling complex (herein also called the RKS signaling complex)
- 30 comprising molecules of RKS proteins, ELS (Extracellular Like SERK) proteins, NDR/NHL proteins and SBP/SPL (Squamosa Binding Protein) proteins, and the corresponding protein ligands (see for example table 3) whereby each of these proteins interplay or act in such a way that modifying genes, or modifying
- 35 expression of genes, encoding ELS, RKS, NDR/NHL or SBP/SPL, proteins or said ligands may lead to functionally equivalent results (Figure 5. Two-hybrid interaction experiments have for example shown in vitro interaction between RKS 0 and
- 40 NDR0/NHL28 and members of the SBP/SPL family. Here we show that in vivo the individual components of this signaling

complex are regulating identical processes, as based on functional genomics on transgenic plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex. ELS gene products  
5 are derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signalling sequence at the N-terminal end. Therefore  
10 these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologues have been detected in other plant species (see list on page 3). ELS proteins are involved in the heterodimerizing  
15 complex with the RKS transmembrane receptor at the outer membrane site. ELS molecules are either in competition or collaboration with RKS molecules involved in the high affinity binding of the ligand. The signal transmitted from the ligand onto the RKS proteins is then transporter over the membrane  
20 towards the N-terminal site of RKS protein, located on the other site of the membrane. The activation stage of the RKS molecule is changed, as a result of transphosphorylation by dimerizing receptor kinase dimerizing partners. Subsequently the signal is transmitted to other proteins, one family of  
25 such proteins is defined as the SBP/SPL family of transcription factors, the other family of proteins is represented by the NDR/NHL members.

The different obvious phenotypes created by modifying the  
30 RKS gene products could be effected by one process regulating all different effects in transgenic plants.

All the phenotypes observed can be effected by the process of brassinosteroid perception. In chapter 1, RKS genes  
35 are clearly involved in plant size and organ size. Loss of RKS expression results in a dwarf phenotype, similar as observed with brassinosteroid synthesis mutants. It was already known in literature that the phenotypes observed from modifying the

RKS genes are also observed when modifying the brassinosteroid pathway genes and/or their regulation, thereby altering the amount and nature of the brassinosteroids in plants.

Literature which describes the phenotypic effects of modifying  
5 the brassinosteroid pathway can, amongst others, be found in:  
Plant Journal 26: 573-582 2001; Plant Journal 1996 9(5) 701-  
713, genetic evidence for an essential role of  
brassinosteroids in plant development; J. Cell Biochem Suppl.  
21a 479 (1995) ; Mandava 1988 Plant growth-promoting  
10 brassinosteroids, Ann. Rev. Plant. Physiol. Plant Mol. Biol.  
39 23-52; Plant Physiol 1994 104: 505-513; Cell 85 (1996) 171-  
182; Clouse et al. 1993 J. Plant Growth Regul. 12 61-66;  
Clouse and Sasse (1998) Annu. Rev. Plant Physiol. Plant Mol.  
Biol 49 427-451; Sasse, Steroidal Plant Hormones. Springer-  
15 Verlag Tokyo pp 137-161 (1999).

It is thus believed, without being bound to any theory,  
that modification of the RKS genes will result in a  
modification of the brassinosteroid pathway, thereby giving  
the various phenotypes that are shown below.

20

"Functionally equivalent" as used herein is not only used  
to identify the functional equivalence of otherwise not so  
homologous genes encoding ELS, RKS, NDR/NHL or SBP/SPL  
proteins, but also means an equivalent gene or gene product of  
25 genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins in  
*Arabidopsis Thaliana*, e.g. identifying a homologue found in  
nature in other plants or a homologue comprising a deliberate  
nucleic acid modification, such as a deletion, truncation,  
insertion, or deliberate codon substitution which may be made on  
30 the basis of similarity in polarity, charge, solubility,  
hydrophobicity, and/or the amphipathic nature of the residues as  
long as the biological activity of the polypeptide is retained.  
Homology is generally over at least 50% of the full-length of  
the relevant sequence shown herein. As is well-understood,  
35 homology at the amino acid level is generally in terms of  
amino acid similarity or identity. Similarity allows for  
"conservative variation", i. e. substitution of one

hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Deliberate amino acid substitution may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. In a preferred embodiment, all percentage homologies referred to herein refer to percentage sequence identity, e.g. percent (%) amino acid sequence identity with respect to a particular reference sequence can be the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, without considering any conservative substitutions as part of the sequence identity. Amino acid similarity or identity can be determined by genetic programs known in the art.

'Plant cell', as used herein, amongst others comprises seeds, suspension cultures, embryos, meristematic regions, callous tissues, protoplasts, leaves, roots, shoots, bulbs, gametophytes, sporophytes, pollen and microspores. A target plant to be modified according to the invention may be selected from any monocotyledonous or dicotyledonous plant species, such as for example ornamental plants, vegetables, arable crops etc. 'Dicotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has two or more free or fused cotyledons. 'Monocotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has one cotyledon. 'Angiospermae' or flowering plants are seed plants characterized by flowers as specialized organs of plant reproduction and by carpels covering the ovaries. Also included are gymnospermae. Gymnospermae are seed plants characterized by strobili as specialized organs for plant reproduction and by naked sporophylls bearing the male or female reproductive organs, for example woody plants. 'Ornamental'

plants are plants that are primarily in cultivation for their habitus, special shape, (flower, foliage or otherwise) colour or other characteristics which contribute to human well being indoor as cut flowers or pot plants or outdoors in the man made landscape, for example bulbous plant species like *Tulipa*, *Freesia*, *Narcissus*, *Hyacinthus* etc. 'Vegetables' are plants that are purposely selected or bred for human consumption of foliage, tubers, stems, fruits, flowers or parts of them and that may need an intensive cultivation regime. 'Arable crops' are generally purposely bred or selected for human objectivity's (ranging from direct or indirect consumption, feed or industrial applications such as fibers) for example soybean, sunflower, corn, peanut, maize, wheat, cotton, safflower and rapeseed.

The invention provides a method for modulating a developmental pathway of a plant comprising modifying a gene encoding for a gene product or protein belonging to a developmental cascade or signaling complex comprising modifying at least one gene encoding a gene product belonging to the complex of RKS proteins, ELS proteins, NDR/NHL proteins, SBP/SPL proteins and ligand proteins. In one embodiment, the invention provides a method for modulating or modifying organ size. Plant or plant organ size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex with a method according to the invention is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating

cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth,

5 proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Use of a method according to invention for elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase for example the size of plant

10 organs, the growth rate, the yield of harvested crop, the yield of total plant material or the total plant size. Decreasing the levels of endogenous RKS gene product is provided in order to decrease the size of plant organs, the growth rate, or the total plant size.

15 In another embodiment, the invention relates to cell division. The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery

20 are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides

25 herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and

30 RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an

35 eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes,

especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

5

In a further embodiment, the invention relates to the regeneration of apical meristem. Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*. Herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of such a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression cassettes in the plant genome. A further example of essentially identical functions for for example ELS1 and RKS0 overexpressing plants is for example shown in the detailed description, example 3, where both transgenic constructs are able to induce the

30  
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regeneration capacity of in vitro cultured *Arabidopsis* callus. Another example comprises functional interaction between RKS and SBP proteins which was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter. At the tip of double overexpressing plants, embryostructures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signaling cascade, resulting in the reprogramming of developmental fate of a determined meristem. Furthermore, it is herein also shown that several RKS genes are able to regulate proper identity and development of meristems and primordia. The invention for example also relates to fasciation, Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific

promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An  
5 example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers  
10 resembling the *Umbelliferae* type.

Identical phenotypes can be observed when transgenic plants are produced that contain the NHL10 cDNA under control of an enhanced 35S promoter. The resulting phenotype of the resulting flowers show that flower organ primordia are  
15 switched in identity, similar as observed for RKS10 and RKS13. These meristematic identity switches are normally never observed in *Arabidopsis* and the fact that two different classes of genes are able to display the same phenotypes in transgenic plants is a clear indication for a process in which  
20 both members of the RKS and the NDR/NHL families are involved. The invention also relates to root development. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical  
25 meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development  
30 that can be manipulated by modification of the levels of RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein  
35 belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular

wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

In a further embodiment, the invention relates to apical meristem identity. All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue

and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering. Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows the formation of completely new types of flowers and fused fruitstructures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

In another embodiment, the invention relates to male sterility. Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Furthermore, surprisingly we observe that NDR NHL gene products share homology with the family of syntaxins, involved in vesicle transport, positioning of cell wall formation and cytokinesis.

Table 1

Homology between members of the syntaxin family and the NDR  
NHL family

5 NHL10= At2g35980

maaeqplnga fygpsvpppa pkgyyrrghg rgcgccllsl fvkviisliv ilgvaalifw  
livrpraikf hvtdasltrf dhtspdnrlr ynlaltvpvr npnkriglyy drieahayye  
gkrfstittlt pfyqghkntt vltptfqqqn lvifnagqsr tlnerisgv ynieikfrrl  
vrflgdlkf rrikpkvdcddlrplstsn gttttstvfvp ikcdfdf

10

Atlg32270 syntaxin,

MVRSNDVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR FEATVYYMNQ  
RLGAVPMPLE YLGSKNTMLL RALFEGQTLV LLKGNERKKF EDDQKTGVYR IDVKLSINFR  
VMVLHLVTWP MKPVVRCHLK IPLALGSSNS TGGHKMLLI GQLVKDTSAN LREASETDHR  
15 RDVAQSKKIA DAKLAKDFA ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS  
QEQRVLMESR RQEVLLDNE ISLNEARIEA REQIQEVKH QISEVMEMFK DLAVMVDHQQ  
TIDDIDEKID NLRSAQAQK SHLVKASNTQ GSNSSLLFSC SLLFFFLSG DLCRCVCVGS  
ENPRLNPTRR KAWCEEEDEE QRKKQKKKT MSEKRRREEK KVNKPNGFVF CVLGHK\*

20

Below the homology is shown between NHL10 (Upper line) and a  
syntaxin protein. (bottom line). The identical amino acids are  
shown in the middle line.

25

IVRPRAIKFHVTDASLTRFDHTSPDNILRYNLALTVPVRNPNKRIGLYYDRIEHAHAYYEG  
VR KF V DA LT FD S N L Y L L RN IG YDR EA YY  
MVRSNDVKFQVYDAELTHFDLESNN-LQYSLSLNLSIRNSKSSIGIHYDRFEATVYYMN

30

KRFSTITLTPFYQGHKNTTVLTPTFQQQNLVIFNAGQSRTLNAERISGVYINIEIKFRLRV  
R FY G KNT L F GQ LV GVI I K  
QRLGAVPMPLE YLGSKNTMLLRLALFEGQTLVLLKGNERKKFEDDQKTGVYRIDVKLSINF

35

RFKLGLDKFRIKPKVDCDDLRLPLSTSNNGTTT  
R L KP V C L PL T  
RVMVLHLVTWPMKPVVRCH-LKIPLALGSSNST

That syntaxins and NDR/NHL genes share large homology becomes even more clear when performing a database search using the following site:

[http://mips.gsf.de/proj/thal/db/search/search\\_frame.html](http://mips.gsf.de/proj/thal/db/search/search_frame.html)

5 searching for homologous sequences with the sequence At1g32270

gene code:

predicted function:

	At1g32270 syntaxin, putative	Syntaxin
10	At5g46860 syntaxin related protein	Syntaxin
	AtVam3p (gb AAC49823.1)	
	At4g17730 syntaxin	Syntaxin
	At5g16830 syntaxin homologue	Syntaxin
	At3g11650 unknown protein	Putative syntaxin
15	At2g35460 similar to harpin-induced protein	Putative syntaxin
	At5g06320 harpin-induced protein-like	Putative syntaxin
	At2g35980 similar to harpin-induced protein	Putative syntaxin
	At1g65690 hypothetical protein	NDR HNL
	At4g05220 putative protein	Putative syntaxin
20	At3g05710 putative syntaxin protein	Syntaxin
	AtSNAP33	
	At2g27080 unknown protein	NDR HNL
	At3g52470 putative protein	Putative syntaxin
	At1g61760 hypothetical protein	Putative syntaxin
25	At5g21130 putative protein	NDR HNL
	At3g52400 syntaxin-like protein synt4	Syntaxin
	At2g35960 putative harpin-induced protein	Putative syntaxin
	At5g06330 harpin-induced protein-like	Putative syntaxin
	At5g26980 tSNARE	Syntaxin
30	At5g36970 putative protein	Putative syntaxin
	At3g44220 putative protein	Putative syntaxin
	At3g03800 s-syntaxin-like protein	Syntaxin
	At2g35970 putative harpin-induced protein	Putative syntaxin
	At4g09590 putative protein	Putative syntaxin
35	At4g23930 putative protein	
	At1g61290 similar to syntaxin-related protein	Syntaxin
	At3g11660 unknown protein	Putative syntaxin
	At1g54540 hypothetical protein	Putative syntaxin
	At3g24350 syntaxin-like protein	Syntaxin
40	At5g22200 NDR1/HIN1-like	NDR HNL

	At1g11250 syntaxin-related protein At-SYR1	Syntaxin
	At5g53880	
	At3g11820 putative syntaxin	Syntaxin
	At3g54200	Putative syntaxin
5	At5g05760 t-SNARE SED5	Syntaxin
	At5g53730	Putative syntaxin
	At4g03330 SYR1-like syntaxin 1	Syntaxin
	At3g47910	
	At5g08080 syntaxin-like protein	Syntaxin
10	At5g11890	Putative syntaxin
	At1g17620	Putative syntaxin
	At2g22180	Putative syntaxin
	At5g22870	Putative syntaxin
	At2g46300	Putative syntaxin
15	At2g27260	Putative syntaxin
	At4g01410	Putative syntaxin
	At5g22200	Putative syntaxin
	At4g01110	Putative syntaxin
	At3g52460	Putative syntaxin
20	At3g26350	Putative syntaxin
	At1g08160	Putative syntaxin
	At2g01080	Putative syntaxin
	At5g56050	Putative syntaxin
	At3g20600	Putative syntaxin
25	At3g20590	Putative syntaxin
	At4g39740	Putative syntaxin
	At1g32270	Putative syntaxin
	At1g13050	Putative syntaxin
	At5g45320	Putative syntaxin
30	At3g20610	Putative syntaxin
	At4g26490	Putative syntaxin
	At5g42860	Putative syntaxin
	At1g45688	Putative syntaxin
	At4g26820	Putative syntaxin
35		

40 This observation provides the explanation for understanding  
the mechanism by which the RKS / NDR-NHL complex functions.  
Cell wall immobilized RKS gene products (containing the

extensin-like extracellular domain) respond to a local ligand signal, in combination with the heterodimerizing ELS protein (s) either as homodimers, as RKS heterodimers or in combination with the heterodimerizing ELS protein(s).

5        Predicted ligands for the RKS / ELS receptor binding consist of peptide ligands (based on the LRR ligand binding domain of this class of receptors). These ligands are normally produced as a pre pro protein. The N-terminal signal sequence is removed by the transport through the Golgi system and  
10        allows modification of the ligand at this stage (e.g. glycosylation). The ligands can then be secreted after which further processing is possible (e.c. proteolytic cleavage, removal of sugar groups etc.) The resulting peptide, possible  
15        transmembrane receptor complex with high affinity, resulting in transmission of the signal from the ligand through the transmembrane receptor component towards the other site of the membrane.

One class of ligands interacting with the RKS and / or ELS  
20        receptors consists of the family of pre(pro)proteins shown hereunder in table 3.

Table 3 Ligands within the RKS signaling complex (herein also called RKS/ELS ligand proteins)

- For each ligand (A to N) the genomic structure before splicing and processing 5'- towards 3' is given. Exons are indicated in large letters; introns and surrounding sequences (including leader 5'-and trailer sequences 3'-) are indicated in small letters.
- Beneath each DNA sequence the amino acid sequence of the pre-pro-peptide is given. The first line represents the signal sequence
- The second (set of) lines represents the pro-peptide.
- The last line represents the conserved Cysteine motif.

#### A. At1g22690

15  
1 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat  
61 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac  
121 ataaactacc aaagtatcaa gctaattgtaa aaattactct catttccacg taacaaattg  
181 agtttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcac  
20 241 ctccgaaaaa agggaaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca  
301 aatgcaatct ataactctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag  
361 cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa  
421 gtatgtgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc  
481 aaaatcacta ctcaagaaat ATGAAGAAGA TGAATGTGGT GGCTTTTGT ACCTGTATCA  
25 541 TCTCTTTTCT TCTGCTTTCT CAGgtaaact gttaaaacca ttttcaagac taccttttct  
601 ctattttcaga caaaccaaaag taaaacaatg aaaaatctct ctggtcttct atagGTACTT  
661 GCAGAGTTGT CATCATCCAG CAACAATGAA ACTTCCTCTG TTTCTCAGgt aagagtgata  
721 caaaaacata ctaaacaaac tttcaagaga gtaatatata aggaatgtt ggcttctttt  
781 ttttgttgct aatcagACGA ATGACGAGAA CCAACTGCG GCGTTAAGA GAACATACCA  
30 841 CCATCGTCCA AGAATCagtt agtctactct ttcaacactc taattccttt gttctaagta  
901 ttttttttgc cccccacaac ctttttttta ttaaatgagc caatttttat agATTGTGGG  
961 CATGCATGCG CAAGGAGATG CAGTAAGACA TCGAGGAAGA AAGTTTGTC CAGAGCCTGT  
1021 GGAAGTTGTT GTGCCAAGTG TCAGTGTGTG CCGCCGGGAA CCTCCGGCAA CACAGCATCA  
1081 TGTCCTTGCT ACGCCAGTAT CCGTACACAT GGCAATAAAC TCAATGTCC TTAaaagact  
35 1141 tctcatttct caactatagt ctcatcttct gattatgttt cttcttttgt tatgttgcat  
1201 gtgtgatgtg tgagcttatt attatgttga ttgttgacat aattcaacta tataatttgt  
1261 atcgattccg aataataaga tgagtgtatt tattggctat taagtttttt tttttttttt  
1321 ttgggcacaa tggctattaa gttttaaaca tctgatttta ttggttacaa aaaaacaaca  
1381 agtttcattt tcatattaac acaaaatctc catcacatatt accaaaccaa aaaaatacac  
40 1441 aaggggggaga gagaccaacg gttcttgggt cagagtgttc atcttgtttg agccgtcacc  
1501 gtttcttaga ctttaacagcc acaacacctt tataaagctt cagcgatcc ttcaacgcac  
1561 ctgcgcgagg ccgagccacc ttattgtttg gatcaaacaa caaaacttct tcaaacgcac  
1621 tcaatgccaa aggc

45 MKKMNVFAVFTLIISFLLLSQVLA

ELSSSSNNETSSVSQTNDENQTAAFKRTYHHRPRIN

CGHACARRCSKTSRKVKCHRACGSCCAKQCVPPTSGNTASCPCYASIRTHGNKLKCP\*

50

**B. At1g74670**

5           1 gaaaaaaaga agaaaagata atggtccgta ttaatatagt tgaaaacttg aaactacttt  
61 ttagtttgta tataatacag tagactaggg atccagttga gtttctttct ttattttgag  
121 ttgtgtttta tgtttgattt tacgttttta tatgtaaata agatatttta cgaattatgy  
181 ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat  
241 aaagtaatat aatataatga ccgttatata cttattgtac atgtgaatga ggaagcttac  
301 acacacacac cttctataaa tagctgacaa aactgyttgt tacacacaac acattcataa  
10       361 atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc  
421 tctctcaaga gctagtcATG GCCAAACTCA TAACTTCTTT TCTCTTACTC ACAATTTTAT  
481 TCACCTTCGT TTGTCTCACT ATGTCAAAAG AAGCTGAGTA CCATCCAGAA AGTgtaagtt  
541 tttatttttt ggtaaaatag aaagtgttaag ttttataatt cattcaatty tttttgcctt  
601 tcccttttcta ttatttgcta taaatctaata acccgcggtta aaattttgttt tgaatttttaa  
15       661 cagTATGGAC CAGGAAGTCT GAAATCATA Cgtaagtaaa aacttcttct tcttttatga  
721 atcttggttc ttattatata tcaataaaaa actcgattat catgattgca gAATGTGGAG  
781 GACAATGCAC AAGGAGATGT AGCAACACAA AGTATCATAA GCCATGCATG TTCTTCTGCC  
841 AAAAGTGTG TGCTAAATGC CTTTGTGTCC CTCCAGGCAC GTACGGCAAC AAACAAGTGT  
901 GTCCTTGTTA CAACAACCTGG AAGACTCAAC AAGGTGGACC AAAATGTCCA TAAacaaaaa  
20       961 cattgagaga gaaaccccaa tctgtttcct attttattta attatttcca gbatgctttt  
1021 gttgtcgtga tggttaaatt atagtgtttt tgcagggtatc atttatcatc gataaacaat  
1081 atcatataaa atcttctatg tttctttcac gttttgtttc ttttggtgta gtcaatacac  
1141 gaaatgtgta tggaccttct aattaggaat atataaaatt ttattttatta attagataat  
1201 ctttcgtata gttaaaattc caaggattac ttttgattcg tttgggacaa tctattttat  
25       1261 attttacttt ctaagtttgt ataactatat cttaaaagtg ttgagacagag tcctaattgat  
1321 tttagtataa ttgttactat ttagttacgc ttcgaaaatt tggaaacttt ccaaagtggg  
1381 ctatatcaat ttgattcact aatctgcgct tccttctagt tttttacaat tatggagatt  
1441 tttcgacgat gat

30

MAKLITSFLLLTILFTFVCLTMS

KEAEYHPESYGPGSLKSYQ

35

CGGQCTRRCSNTKYHKPCMFQCQKCAKCLCVPPGTYGNKQVCPYNNWKTQGGPKCP \*

C. At1g75750

5           1 cacaactttt atacgcacca ccaaccgacc cattttgaaa aagagaaaat aaaccacaaa  
61 aacacacata aataatatgc tgataacaat gtcttaaaaa tctatttacc atttctagta  
121 atcaatatct attgcaaaaa atatttataa gaatacaaat gaaaaatgat aaaatacaaa  
181 tgattttctca attacctaata aaatataaaa atgtcttact ttattttcag ccactgttgg  
241 aaagtacttg caatcataatc gtattttgaa ttataaaaact cagaaacaat tattttccct  
301 gaaaagttaa aacttttaat aagatattta taaaataaaa agaatagtct agaccgaaaa  
10 361 tgggggtcggg tgtccatcca aaggagtgc ataaatagaa ccctccaagt tctcattagg  
421 acacaacaac taaaaccaca tttatcatta cagtctgatt tgagctaagt tctctcatca  
481 taaactctcc ttggagaatc ATGGCTATT CAAAAGCTCT TATCGCTTCT CTCTCATAT  
541 CTCTTCTTGT TCTCCAAC TC CAGGCTG ATGTCgtacg tctttttcat cacaactaa  
601 ttataactca tataataact atgttttcaa aaacatattt ctcacatgtt acaacaatat  
15 661 tcttgagcagGA AAAC TCACAG AAGAAAAATG GTTACGCAAA GAAGATCGgt aattatatga  
721 tttttattaa acctaacggt aaatttagag tgagattaat aatctgtgtt tttctttctt  
781 gtatatatag ATTGTGGGAG TCGGTGTGTA GCACGGTGCA GGCTTTCGAG GAGGCCGAGG  
841 CTGTGTCACA GAGCGTGCGG GACTTGCTGC TACAGGTGCA ACTGTGTGCC TCCGGGTACG  
901 TACGGAAACT ACGACAAGTG CCAGTGCTAC GCTAGCCTCA CCACCCACGG TGGACGCCGC  
20 961 AAGTGCCCAT AAgagaaac aaagctctta attgtgcgg ataatgggac gatgtcgttt  
1021 tgtagtatt tactttggcg tatatatgtg gatcgaataa taaacgagaa cgtacgttgt  
1081 cgttgtagt gtgagtactg tattattaat ggttctattt gtttttactt gcaagttttc  
1141 ttgttttgaa tttgtttttt tcatatttgt atatcgattc gtgcattatt gtattatttc  
1201 aatttgtaat aagattatgt tacctttgag tgggtgttta tcatactttt tttctatggt  
25 1261 aagagggtttt ggaaaagtat cgagaatgat atataaagta attttgatat cgacgcaaga  
1321 tgataactac tagactagct gagtataaga atattgatgt atatatattgc ggacaatttt  
1381 gaatttatta taccattatt taatcacgac catataaaaa taattcttgt ttgcgttata  
1441 atttgtgtta atacgataga gtagacaaat ga

30

MAISKALIASLLISLLVLQIVQA

DVENSQKKNGYAKKID

35

CGSACVARCRLSRRPRLCHRCAGTCCYRCNCVPPGTYGNYDKCQCYASLTHGRRKCP\*

**D. At2g14900**

5           1 ataactaaca atggttgagt ggagatgtgc ttttagtcaa gtggttaaat atatttgact  
61 tctgtttttt cattggagtt tgactctact aagttgtgtt tcctcgcgta gtaagaattg  
121 gttatggatt agaccgtatc gatctaaaga tgtcaaagaa aaaaaaatgt ggttgtgtaa  
181 agtaaatatg tagatttgtg cggattaaag tatgttttga ttcacatcat tattgttatt  
241 ttttcatgaa ttctaaatgt aaagtcttta taatcttatg ttacttttta caaattgtaa  
301 ggattactct gaaatttgyt atcgaattct aagacaaata caaataaaca atgactgaac  
10       361 aagttgataa aacataatgg aaggaataat actgcagttc tattaataac taaagaagtt  
421 ggtagattgg cctataaaag gagaataaag agaccacaag aaggtctatt attcggggac  
481 taaagaaagc caaagaaaac ATGAAATAA TAGTCTCCAT CTTAGTGTTA GCCTCTCTTC  
541 TTCTAATCAG TTCATCTCTT GCTTCGGCTA CTATATCAGg ttggttctaa tctcttcaag  
15       601 aatcttcttc tctctatttt ttttttcttc ataaagttag ttatgttatg attggtttag  
661 gtcacaattg tttctttatg ctttcgtttc cataagaaaa atattacaaa tatttaactag  
721 aacaacataa catgcaaacg agtaatacaa aattcattat tatgatcaaa acaatcatga  
781 attagttgga cttattttgt aaattccgaa aatctcacta aaataaagtg aacttcatct  
841 acatggcttt agacgcaaaa tctttaaggy tatctacaca agtttggaat gaataatttc  
901 ttgcgatggg agtgtagaag gatctagaag atccacaaga tcattagtgt atcttctaga  
20       961 tctttttaca ttgagaagtg aggagatatt tgttgtatta gaaagaatta tagtgaagta  
1021 aattttttta ctatgtacga tcattttatat acgatacttt tattaaggat cttgtggatc  
1081 ttctagATGC TTTTGGTAGT GCGCGGTAG CTCCGGCACC GCAGAGCAAA GATGGACCGG  
1141 CGTTAGAGAA ATGGTGTGGA CAGAAATGTG AAGGGAGATG CAAAGAAGCG GGGATGAAAG  
1201 ATCGGTGTTT GAAGTATTGT GGGATATGTT GCAAAGACTG TCAGTGTGTT CCTTCAGGCA  
25       1261 CTTATGGGAA TAAGCATGAA TGTGCTTGCT ATCGTGACAA GCTCAGTAGC AAAGGCACTC  
1321 CTAAATGTCC TTGAttctat ttctttccaa ccaaaaattt aaataaatga ataagagaga  
1381 tccagtaaac taataataaa ctataaatgg atcttttgtt tatgattttt ttttttcat  
1441 ttctattttt acgaattttg cttggtcttt ttgaagtaag tttttaaata ttgaaaagtg  
1501 ctaaaattat gtggaatcg ataagttaa tgaatgatat aatatataag tcttcagttt  
30       1561 ttgtaagaaa cttgaatata aataatattt catcaaacat aataaataaa tatattgtat  
1621 aattagattg gctcaaccga tataaacaat tgaatcgaat ttttcttctt aaatatataa  
1681 tcatccaaat ttgtattgta ccaatgaatg agatggttat gaggactaga agatagagag  
1741 gagaagaacg tgtttggtaa aataattatg atggagttga gacaactttt aagagatttt  
1801 aaaaagactg actaacgtgt taggttcacg acgt

35

MKIIVSILVLASLLLISSSLASATIS

DAFGSGAVAPAPQSKDGPALKW

40

CGQKCEGRCKEAGMKORCLKYCGICKDCQCVPSGTYGNKHECACYRDKLSSKGTPKCP\*

**E. At2g18420**

5           1 gccaatgggt aactgaggaa gaaggataag accaaaaaaa aaactaaaat ggacagattg  
61 aattagtaaa aagataaatt ctaaaaaccg aaacaaatct taagttgggt tatacacatc  
121 tgcattgacc aacaaaagaa agtagactga aatttatttg aaaatgatct tgtaaaaggca  
181 tattatataat ttaatttagg aaatgaatgt taaatccttt aaattgtttt gatttcacaa  
241 aaggataaag aaatattgggt tacatacatc ttaatgtggt gacccaaaaca aataaaatgt  
10       301 gataagaaac aataaaacca ttttgaccac agttcttata gttttaatat tctttaattg  
361 tcattttgta gtgactaata atattacatt aaacctaatg tataaataga agcccatct  
421 tctacgcctt tataatttagc aacaaccaa aacattcatt tgtcattttg tctcctcttt  
481 tgttttctct gatcactagt ATGGCTGTAT TCAGAGTCTT GCTTGCTTCT CTTCATAT  
541 CTCTTCTGTG CCTCGACTTC GTCCATGCCG ATATGGTGgt acaattttaa caaccaaata  
15       601 tattttctta tttgatttta ttttttcaca acttttgtct acgttctaata ggaatttttt  
661 tcaaaatatt catgcagACG TCGAATGACG CCCCTAAAT CGtaatatc tctatcatat  
721 aaacacgtac gttgaatttc tatatactgt tgtttaattg aagttttggt tggaaattgt  
781 atgtatttgt agattgcaac agcaggtgcc aagagCGGTG CAGTCTTTCG AGTAGGCCAA  
841 ATCTTTGTCA CAGAGCGTGC GGGACTTGCT GCGCTAGGTG CAACTGCGTG GCACCGGGCA  
20       901 CATCCGGAAA CTACGACAAA TGTCGTGCT ATGGTAGCCT AACCACCCAC GGAGGACGCA  
961 GAAAGTGTCC Ttaaaaaactc tgtcgtggtt tgatttgatt tctgttataa tactttactt  
1021 ttatgagagt aattgtggtt attttcttg gaattattaa aaagcaaaag aaagagaatg  
1081 ttatacgtca tgtgcaactc ttcgatcttt gtttagtgt ttatccaatt tgtacttggt  
1141 gggttggttc ctggttaaca ttaggtctga aaaggtattg ttttctatta tacaattcac  
1201 taaataggca tcytacttgc atataaaata aagaatgaag agagaagtaa aagagttttc  
25       1261 tttttttact catggaagt aggcaatggg tttaaatag gtaacaacag aattggaggg  
1321 gacttaatga actatgacgt aaaactgaga gcyattgaat atgtaacgtt accaacaata  
1381 ccaataaaat tatgaagat agtatatgaa attacgttta attaatgttt ccgggttgaa  
1441 tgtattatat atagaagtaa cagtacgatt ttattacat ttttgtaaa gattcctaga  
30       1501 aaggataaac ctctataaag ttaataatag tcttgagtct tgactcttcg aggcataata  
1561 attcacgcga taattaatcg ttcaactatt attctatatt ctatataaca tgagcttcaa  
1621 caaaagaagc atcaatcata tcttcaacag tatactgcag tgtaatgtaa catattcaag  
1681 atcaaacggg acaaaaaagc aagataccgt cgaaacaatc aaaccccatg tatcataaac  
1741 tcccatcttc tctttcctaa attccccgtc gcttgcaaa tc

35   MAVFRVLLASLLISLLVLDVHA  
DMVTSNDAPKID  
CNSRCQERCSSLSSRPNLCHRACGTCCARCNCVAPGTSIGNYDKPCYGLTTHGGRKCP\*

40

F. At2g30810

5           1 cttttatttg tttgtgaaaa aaaacaatag cttttatttg tcctaggaat tatttaatat  
61 attaaataac agctattttt ctcttatttc ttagtgatta aaatatttaa aatacagacc  
121 aaaatttaatt gtttatgtta atatatattac tccttaatcc ttatatatta aattgtataa  
181 tgcattgtagt taataaattg ttttccaaaa ttcattcata attttattcc taaattattt  
241 tggtaagaa aacacatctt tgaataatta aatgcttcct tgtatttgat aatttcttga  
10       301 tattttaaaa taccttctat actatgccaa tgttattggt tataaatagg tttaacattg  
361 atcctgaaat atatcataag aaaatcaaaa gtgaaataag agatcaaaAT GATGAAGCTC  
421 ATAGTTGTCT TTGTTATATC CAGTTTGTG TTTGCTACTC AATTTTCTAA Tgtaaaaatt  
481 attattattt tcttcatatt atgatttatg aattcagaga aataaagttt ttttttttat  
541 gtgtgtatgt acagGGTGAT GAATTAGAGA GTCAAGCTCA AGCACCTGCA ATCCATAAGg  
15       601 tatattttaa ttataaaata tcaataactg aataataaat aataaatata ttacaacaag  
661 aatatcaatg ttatttttca aactacataa ttttaaaata ttttattgat aacacaaatg  
721 tatattatta tcgtctccat tgatttgcac tctaaatttg tttttgttat ccaaccaatt  
781 tcagAATGGA GGAGAAGGCT CACTTAAACC AGAAGgtaaa ttgtttaaaa gatattattt  
841 ttatttatat agtaaatgat tgatcaaatc acaacttaaa taatttaatt gttgatttat  
20       901 atttttctga agAATGTCCA AAGGCATGTG AATATCGATG TTCGGCGACA TCTCACAGGA  
961 AACCATGTTT GTTTTTTGC AACAAATGTT GTAACAAATG TTTGTGTGTA CCATCGGGAA  
1021 CATATGGACA CAAAGAAGAA TGTCTTGCT ACAATAATTG GACGACCAAA GAAGGTGGAC  
1081 CAAAATGTCC ATGAAAACAA aaaattgtaa aagcaaaata aaatctatcg ttgttatctc  
1141 tcaataaaat ctatgtttgt aatccttgtt tttcaatata gaatataata tggagttttc  
1201 ataatttctt ctattacaaa attaaagtta atgcacaaat aaattgaagg gacttggacc  
25       1261 ttttcgtgta agttctttct ttaaatcacg aacaatttag atttatattt tcaactttac  
1321 aaacacaaaa catggatgct ctttaactct catccaaaca aaatgcattt ctctctttct  
1381 ttttctaaac atttcacaac aatatcccat attatatcta agatatatga tctttttaaa  
1441 ttgaatttat ttaggccatg ttttaaaatc gtgtttggtt agattgacct atgaaatggt  
30       1501 gacatatttt aacattccta aatatgacta aaaatgatta aagatatatta ataatatatt  
1561 tgctctatta aaaatgatta aataaataat aata

MMKLIVVFVSSLLFATQFSNG

35

DELESQAQAPAIHKNGGEGSLKPEE

CPKACEYRCSATSHRKPCLFNCNKKCNKCLCVPSGTYGHKEECPCYNNWTTKEGGPKCP\*

40

**G. At2g39540**

1 taatgctata cttttaatct ataatatata ttagatgtga cttaaggaat ttcaatagtt  
5 61 atacataata ataaaaatga atatttgta gtgttacaaa ctgtgtgtca taatcatcat  
121 tcatcaggat ttcaaaaata tctcaaaatt gttgtaagtt catgtaattc gaaatgaatg  
181 tgcactataa gaaataaatt tacaatttaa aaaatgcttc aatactggtt acaaaaaaaaa  
241 ctttcaatac tagtattata ctacttactt agtcaaaaaa gtttatgaat atgggttttt  
301 ctgtatgtta atatttttaa ctgaaaatag taccgacata acaagtaaag atatctttat  
361 ttaaagtaac aaacattaat ttcaacttcaa attctcacta ttaaggattc ctctctttgt  
10 421 agccacattt caccatcact actttgtttt cgcatacttt taaattttgt atacgtagca  
481 aactctttcg agaaaacaag ATGAAGCTCG TGGTTGTACA ATTCTTCATA ATCTCTCTTC  
541 TCCTCACATC TCATTTTCT GTACTTTCAA GTGCTGATTC GTgtaagtg ttacttaatc  
601 tagttaataa ttgtaggtca tgcattgtatc attttgaac aagttttctg aaatttctaag  
661 attttacata tatatgtgat aaatgaatta gcagCATGCG GTGGAAAGTG CAATGTGAGA  
15 721 TGCTCAAAG CAGGACAACA TGAAGAATGC CTCAGTACT GCAATATATG TTGCCAGAAG  
781 TGTAAATTGTG TTCCTTCGGG AACTTTTGA CACAAAGATG AATGTCCTTG CTACCGTGAT  
841 ATGAAAAACT CCAAAGGTGG ATCCAAGTGT CCTTGAacgt tctttgaaga tcctcatcac  
901 atacataaa cttctacgta ctatatgtgt ggaaatatta atcacattct atgtttgaaa  
961 tatataaaat aaaatcaatg cccccaatgt tggaaatctt caatgtgata tcttaatata  
20 1021 tatcacgaat aaaaaagttt aaattttctca atctcatttt taatctttta tctaatttct  
1081 taacacatca acgaatcttt aatctttaat catgtagata attatcagag cacctaaca  
1141 ttgcgcggtt ttgtgattat acaagtaac atcgtgctgt ttttgacttt tgaaaaccac  
1201 agatccaaaa actgtttact ttctcttaag agaaagcaaa gccgagttag tccaagcgag  
1261 ttttgagaga ttctgtgact cactaccgga gaacgacgct atgtcagaga ccgccgtgtc  
25 1321 aatcgattcg gaccgatcta agtcggagga agaagacgaa gaagagtatt ctccac

**MKLVVVQFFIISLLLTSSFSVLSSA**

30

**DSS****CGGKCNVRCSKAGQHEECLKYCNICQKNCVPSGTFGHKDECPCYRDMKNSKGGSKCP\***

35

H. At3g02885 (GASA5)

5           1 cgctttctat tacacttttt tttcttttta gtcgcacttc acaattagct taattaattt  
61 cctaaactcg cttatttttc cctttctata tacagatatt atcatttagtg acattttcat  
121 tttccaaaca gagcgtttag acactagtca actacacaat ataattttcc aattttcact  
181 gagagaaatg tttttttttt ttttttccaa ggcaagattt tagtcttttg gttctctata  
241 cytgggtaat tagtgattga taatttacac tgttgagtct ttgacattgt ctaagagaca  
10 301 aaaacgacaa gtgtggtacg taattagaaa ttaaaatgac ctacttcccc agaatacagg  
361 catgaacatt ggcaatacca aatttcttga ataccattga aggaaatcca cactaatcat  
421 tttctctata aatatcttta atccgtttta ttgtttctta agaatcattc attgggcaatc  
481 aagatttttt aacaaaaaaa ATGGCGAATT GTATCAGAAG AAATGCTCTT TTCTTCTTGA  
541 CTCCTCTCTT TTTATTGTCA GTCTCCAACC TCGTTCAGgt aaaccactca aaacagattc  
15 601 agtttatata agtctgatat tgaagtttta tatattacag gctgctcgtg gaggtaaaaa  
661 tgaccaaaagg ctatacattc cttaaaaatt taatggctat tagttttctg atattgaagt  
721 tttatatata tatgacagGC TGCTCGTGGT GGTGGCAAAC TCAAACCCCA ACgtacggac  
781 tcaaaacttt tgttgtttca tatgatcata ttaatttatt aatcactaat tattgataat  
841 gttgataaat aaacttttaa gtaacaataa tgggttttat tttgtgaaat gtcagttttc  
20 901 tagtatactg tatgctgtga attataagca tgaacataaa gatctcaatg atttgttttt  
961 tgtttgtttg ttgtgatatg cttttttgat ggaacttca attgtagAGT GCAACTCAAA  
1021 GTGTAGCTTC CGTTGTTTCA CAACATCACA CAAGAAGCCA TGCATGTTCT TTGCTCTCAA  
1081 GTGTTGCAAA AAATGTCTTT GTGTTCTTCC TGGCACTTTC GGCAACAAAC AAACCTTGTC  
1141 ATGTTACAAC AACTGGAAGA CTAAAGAAGG CCGTCCAAAA TGTCCTTAAA acttcttttt  
25 1201 agatataatt gataatattc atctagtttt ggattatcaa acacttacta ctctgtttta  
1261 atctgtttct acaagttggc gatttgtctc tacacttttt ttgtgtcttt tgctcttaac  
1321 tgttgtgttt gttatacgtg taagcccgcc caatgtgtca tggccgaact tattatgggt  
1381 acatatttat gaaatgggct tcattatcaa ttgatttgag cctacaaaaa tgtagccata  
1441 aagcccatat agttgtaatt gttaatattt cagtCataaa tatgattttc tatatctatg  
30 1501 atttatctct agtgttgatg atgtttgtat gtggaagtca tgttctattt gcttccacgg  
1561 tttaaaaacc atcaacttgc taaggtcaaa ttctaataat actgtgaaaa acattattta  
1621 cgtgcgtaat tatatgaatt tatgaatagg ttttaattcc attttttcct aatagtgttt  
1681 tatgtcaaa

35

MANCIRRNALFFLTLLFLLSVSNLVQAA

40 RGGGKLPQQ

CNSKCSFRCSATSHKKPCMEFFCLKCKKCLCVPPGTFGNKQTCPCYNNWKTKEGRPKCP\*

45

I. At4g09600 (GASA3)

1 taggctggca atttaactct gagacgtctt tcttgatat agaataaaac atacgcgtgt  
5 61 aaaagaaaac gcgatgaatcg aatgatgagt gttaacgttc gatcgagatg ccaccaaatac  
121 ttttcattaa aatgaattgt ggaggacata ccacttttaa cgagggtcatt tccactgggt  
181 gacatgtgga ctctactttg ggtggcatgt tcatactctt ccacatcacc atgtaaacgt  
241 gaaaacaccc accacactca cttacatctc aaacacatgt cttcattatc gtacgtagct  
301 ccaaaaaaaa aaatgaaaac taggtttagt gattctattt cgcaatgtat aatatacaac  
10 361 ttgtaaaaat aaaatatttg aataagcatt ataaataaac ccaagaggtt gttagattta  
421 tatacttaat tgtagctact aaatagagaa tcagagagaa tagttttata tcttgacaga  
481 aactgcatgc tttttgagac ATGGCAATCT TCCGAAGTAC ACTAGTTTAA CTGCTGATCC  
541 TCTTCTGCCT CACCACCTTT GAGgttcata acttttgtct ttacttctcc atgaatcatt  
601 tgccttcgtc tatccttaac tcatatgtgt ttgatcaatg ataataatc atcattctct  
15 661 tcagCTTCAT GTTCATGCTG CTGAAGATTC ACAAGTCGGT GAAGGCGTAG TGA AAAATTGg  
721 tatgtaacgc taacatatat gtaaagtgtt atatctctgt ttatatatga tttttaaacg  
781 gttaaaaact agtcataatg gtataaatat atcatgtgaa gATTGCCGTG GGAGATGCAA  
841 AGGTAGATGC AGCAAATCGT CGAGGCCAAA TCTGTGTTTG AGAGCATGCA ACAGCTGTTG  
901 TTACCGCTGC AACTGTGTGC CACCAGGCAC CGCCGGGAAC CACCACCTTT GTCCTTGCTA  
20 961 CGCCTCCATT ACCACTCGTG GTGGCCGTCT CAAGTGCCCT TAAacatata cacatacaga  
1021 tgtgtgtata tgtcttcgc gagcacacac gtacgtttat gttttaagga caatagtatg  
1081 tatgagcagc tataaacaaa ccagaagtta atggttcacg ttgaactagt ataagttgta  
1141 tgaactgtgc tttttttgaa caaccacttt tgctgtaagt ttagcaaccc tatttaataa  
1201 attagagatt acaaaaaaaa aaatgaaaaa tgtttaaaaa acgtggattt ttaaatattg  
25 1261 gattaaaaat taattttcat tttggttgat ttgtcaataa attagctaag tttgtatac  
1321 taggccgttt aagatatgct gttaaatttt tgataataga gttgccttag aagttcataa  
1381 ctgtaaatat ctaacttcac ttcaatctca caaacacacg aatcaacttc agcactaaga  
1441 atcgaattga ccagaactga aagaaagtaa aagaaaagct gaatacagag aatttaacga  
30 MAIFRSTLVLLLILFCLTTF  
ELHVHAAEDSQVGEVVKID  
35 CGGRCKGRCSKSSRPNLCLIRACNSCCYRCNCVPPGTAGNHHLCPCYASITTRGGRLKCP\*

J. At4g09610 (GASA2)

5           1 ttaacagttt aacaccataa tgttaaactc ggtttagcat tttggtgtaa ttctacctct  
61 ttaaccatac atactaaaga cgcagagaag ttcatatggt agttaatcgt aaatagctaa  
121 actttttaatt gggggttaaca tattatttaa cacttaacat ttaactattg atctctcatt  
181 ttttttttat taaccaaagt aaattcattt tagaaccaaa cgtttcaaaa actcgtaatg  
241 ttttctcatt aaatcttatt tatagctcac acaaagaaaa actacggaca tgcattgacc  
10       301 caattatata catggattat tatttttagt gttataatat gatacaaaat aaaaaacatt  
361 tggatagccg ataggcgata gccactataa atataccaaa gaggttggat tatacatata  
421 gccgtaatac caaagagagt atcagataga aatagttcta atattttgta caactcacag  
481 aaattgcatg agtttcgaac ATGGCAGTCT TCCGAAGTAC ACTGGTTCTG TTAATAATCA  
541 TCGTCTGCTC CACCACTTAT GAGgtttata atatttttg tctttatagt tccccaagaa  
15       601 caccatagcaa tattatactc aattcatgtt tatatgataa tgactgatca ttctcttcag  
661 CTTACAGTCC ACGCTGCTGA TGGTGCAAAAG GTCGGTGAAG GCGTAGTGAA AATCGgtatg  
721 taaccctaac ttatatataa cacgttggtt tataacttaa tattctgatg gggcgactc  
781 tcttcccaac ttatatatat ctttgttatg gagaatgtct caagctttta atgagatgtt  
841 atattctcga gaaggaaact atgaactaaa agctttggat tcctttgcaa caaatataaa  
20       901 cttttgatgg gtttaaacgg attaaattag ttacatgtgt ttgatgaatg tatgtatgat  
961 tgtagATTGT GGTGGGAGAT GCAAGATAG ATGCAGCAA TCTTCGAGAA CGAAGCTATG  
1021 CTTGAGAGCG TGCAACAGCT GTTGTTCCTG CTGCAACTGT GTGCCACCTG GTACTTCTGG  
1081 AAACACCCAC CTTGTCTCTT GCTACGCCCTC CATTACCACT CACGGTGGCC GCCTCAAGTG  
1141 CCCTTAAaat ttcttctgtg tctgtttctg tttctacttc tatttcgaat atatgtacat  
1201 gtgtgtgtac gtgtgtatgt atacaagtac tgctatgttt tggaggacaa aagtatatgt  
25       1261 atgagaagct ataaactaat tagaagttag tggttatgct tattatcaaa ccgtgttact  
1321 tctgaacaac caatttcggt ttgttccaag ttggcaacc ctaaaataaa aattcaaaat  
1381 gattggagac tactcgttta tagacattga aaacgatgaa atctcgttac gtttttatat  
1441 tttttgaact gtaattattat tatgcagaag cggttttgta atgggcccac aaaaaaaaag  
30       1501 tggttttgta atggatattga ttccgatcta ttctggaaat ggtctcaaaa agtagagttg  
1561 agatctcaat acgaaaatga accctttcgt ttgatttatc aaagcctttt attttgaaaa  
1621 cgttaaatcc tcactaggat ctctctt

35   MAVFRSTLVLLIIVCLTTY

ELHVHAADGAKVGEVVKID

CGGRCKDRCSKSSRTKLCLRACNSCCSRCNCVPPGTSGNTHLCPCYASITTHGRLKCP\*\*

40

**K. At5g15230 (GASA4)**

1 aaatatccac cctaaaaatga atctaaaaat gtacaaaatc acaggaaaaat aaaactaagc  
5 61 agaaatgtcc taagaaaact aaagttttta aaaaataatc ttcaaagaga tactccaact  
121 ggtgttataa gcaaaacttg atttatcaaa aacagggtca tagtatttta tatttagtac  
181 tataagcttt ccttaaacca tgtgcaaaac catctaccgc agtctaatta ccaatagcaa  
241 gtaataaaat gggactaaca ttggaggcat acgtggaata atataattgg aggaatacag  
301 taataatgat atgtgttgcc acaggggaata attgatacga gcaaatygt gtatatatag  
10 361 cttatatgca acatcattgg gtcctcaacc aaaaactcct ctctcagtac acttcttttc  
421 atacctcaag agactaaaac tagtttgagg agatttagag gagtggttg tcttttgat  
481 aacaatatcc caaactgaaa ATGGCTAAGT CATATGGAGC TATCTTCCTC TTGACCCCTCA  
541 TTGTCTCTCT CATGCTTCAA ACCATGgtaa cacctctatt attttttct tctttcaatg  
601 tttgaaaata ttgaagataa tatatttgat tgttttcctt attgacgaac gatatgagac  
15 661 aaatgtgggt tctattattg tacttttagt tggaaatata ttaatttagc ctttttaatg  
721 aaattaattt tacttggttt tcctctctct ttttttcggt ttttagGTTA TGGCCTCAAG  
781 TGGATCTAAT GTGAAGTGGG GCCAGgtcag ttttattatt gaatcgacta gtaattacct  
841 tttaaactat attttatacc tattgttatc tcgtaactta acgaaaagtg attaatatgt  
901 tacttttttt ggttaatttt cagAACGTT ATGGACCAGG AAGCCTGAAA CGTACCCgta  
20 961 agttttttct tcacagctat tcttaacaa tttttttta atctcataat cgacgaaaaa  
1021 taaacaattc aagaaatcct ttatttgttt ataataaaaa aaaataagca tttcagttgc  
1081 agaaaaaag ttgaaagtga agtgtaagt ggactgtttg gtcagatccg tagactcaaa  
1141 atatattaga tattgacgaa attgcccctt aatatgggtca tacagtcaaa gcaaccact  
1201 atcttgagac ccacaaaaa gtaaaaaaaa aagctaata atttccacta gattctgttg  
25 1261 tttttattag taataaaaaa tttttgagt ttaacatttt gatattgttt gtatttgaaa  
1321 caaccagAAT GCCATCGGA ATGTGATAGG AGGTGTA AAA AGACACAGTA CCACAAGGCT  
1381 TGCATTACGT TCTGCAACAA ATGCTGCAGG AAGTGCTCT GTGTGCCTCC GGGTFACTAT  
1441 GGAACAAC AAGTTGCTC CTGCTACAAC AACTGGA AAA CTCAGAGGG TGGACCAAAA  
1501 TGCCCTTGAA aaaaatctccc ttcgttccc ttttataata aaaattttca actataacta  
30 1561 aatttccttt gatcaatggt ttatctactt tattcctaatt gttgtaatgt tatgtcactc  
1621 cttttcggt tttgttctaa atcctaaaaa aaatgagagt ggcctatga atgatatttt  
1681 tcataaatac ttgtgtttct aaagatatatt tcccattcat ccacaaaaa aaaagatatt  
1741 ttccatttcg aaaaatagtaa tactataaag gtaaggcaa accaaataat acaatttaaa  
1801 aaattcctgc gaaagaagta tgcataatga gaaaagagt acattgggtc tctcgccca  
35 1861 gtactaaaaa gccattatt gatttttcca agctttttac aaaatcacgt gttctaacgc  
1921 gattgctttt tgcgcaatc ttcttttata caagacttgg gctttgggca gttggaata  
1981 aataacgaca acgatatttt acaatcgg

MAKSYGAIFLLTLVLFMLQTMV

40

MASSGSNVKWSQKRYGPGSLKRTQ

CPSECDRRCKKTQYHKACITFCNKCCRKCLCVPPGYGKQVCSCYNNWKTQEGGPKCP\*\*

45

L. At5g14920

5           1 ttgctcactg gtgcaataat cgaagtgaag agcctcttta tatgaaatat ataagcgaca  
61 cagccttatg ggcataatcga atgctatttta tttatttgat aagaagatta ataatttcaa  
121 tttgtcatcc actagtctct tggggtactc aaaacatata accaaaaagt ccatagagtt  
181 atttggtctt atttactgat aaagtattcc aagttgatgt acgaataaag tggcaatttc  
241 atgtattatc aatataatcc atttttggga atctgatatt ttgtttatcc tcgagctctg  
301 agagatatat tttggtgcag tgaaggttca aagctggcat gcatgatgca tataataact  
10       361 gctctggacc taatacttac tacgcattta aattaatatt tatggataat atggttaata  
421 aataaggaac ttctatttat atcacaaaag gtcactggtc ttcttctgtt gacttcacca  
481 ctttctcatc tcccacaaaa ATGGCTCTCT CACTCTTTC AGTCTTTATC TTTTTCATG  
541 TCTTTACCAA Tgtaagttat tcttactttt cataacaaaa ggtgttatta tgttaaagac  
601 tacataatat tatacaatta tgtgcattac gttttcgcgt attgtaacta actatgtatt  
15       661 ttgattatcc accgagcagG TTGTTTTTGC TGCTTCAAAT GAGGAATCCA ACGCCTTAGt  
721 acgttttcta atttccagtt taattatttc tatgcgtctt taactatata ctccaggcatt  
781 tttattgtatt attgtgtatg aagttaaatt ttggtatatg ttgtatttaa atttatagGT  
841 TTCTTTACCA ACGCCAACAC TTCCATCGCC ATCTCCGGCT ACCAAACCGC CGTCGCCAGC  
901 TCTCAAACCG CCGACGCCGT CGTACAAGCC ACCCAGCTG CCAACTACTC CTATTAAACC  
20       961 ACCCACCACA AAACTCTCCG TCAAACCTCC AACTATTCCG GTTACACCAG TAAAACCTCC  
1021 GGTFTTCAAT CCTCCGATCA AACTACCGCC GGTACAACCA CCTACGTACA AACCCCAAC  
1081 GCCAACAGTT AAACCACCGT CCGTCCAACC ACCTACGTAC AAACCCCAAC CTCCAACGGT  
1141 TAAACCAACC ACTACATCAC CGGTAAACCC ACCCACTACG CCACCAAGTC AATCACCGCC  
1201 GGTCCAACCA CCTACGTACA AACCCCAAC GTCACCGGTT AAACCAACCA CCACAACCTC  
25       1261 ACCGGTTAAA CCCCCACCA CGACGCCACC GGTCCAACCA CCTACGTACA ATCCCCAAC  
1321 TACACCGGTT AAACCACTA CAGCGCCGCC TGTCAAACCT CCAACACCAC CTCCCGTAAG  
1381 AACTCGGATA Ggtaataata attttctttc aaaagtgtga tgattatcgy tcggttgatta  
1441 gatcggatgt ataattggac taaatttttg acggttttag TTGCGTGCCT TTATGTGGGA  
1501 CGAGGTGTGG GCAACACTCG AGGAAGAAGC TATGTATGAG AGCGTGCCTC ACGTGTCTGT  
30       1561 ACCGTGCAA GTGTGTCCC CCAGGCACCT ACGGTAAATA GGAGAAGTGT GGATCTTGT  
1621 ACGCCAACAT GAAGACACGT GGTGGAAAT CCAATGTCC TTGAaccttt atatgacgat  
1681 ggttggttaaa cgaataaatt taaatcaatg gagtttttat aagtttgtaa tgcgtttgtt  
1741 ttgtttatag taatattgag ttggatcttt gttacggga cgtagaatac taaataatga  
1801 aaaaaacctt ctcgatgaat taagggtttt atgaatttgt ttgtattga ataataatag  
35       1861 gatggataaa gttttattat tctaacaggt tactttatta ggcatttctt cggctcatgt  
1921 aactcttgta tcgctgaaac tatgtaatag atagaagaac ctaaaaaag aaagaaaaca  
1981 agaaatgcac atagcgaagc tcaaaagatg agtgttctgc tagcggtaat gttgttattc  
2041 agttgggtca aatgctctaa ttgcaaatct tatttgggcr ttatatagac tcttatgtgc  
40       2101 atatggtcca gcctatttgg gccgatgtgt ttgaagatca tttgggaaag tcttgcgcaa  
2161 ggag

MALSLLSVFIFFHVFNTNVFAAS

45       NEESNALVSLPTPTLPSPSPA  
TKPPSPALKPPTPSYKPPTLP  
TTPIKPPTTKPPVKPPTIPVT  
PVKPPVSTPPIKLPPVQPPTY  
KPPTPTVKPPSVQPPTYKPPT  
50       PTVKPPTTSFVKPPTTPPVQS  
PPVQPPTYKPPTSPVKPPTT  
PPVKPPTTTPPVQPPTYNPPT  
TPVKPPTAPFVKPPTPPFVRT  
RID  
55       CVPLCGTRCGQHSRKNVCMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTRGGKSKCP\*

M. At5g59845

5           1 gacttgagta tgaatccaat aacccaaaat ttatgcagat tttagaatac ttcttataaa  
61 tctttaaata ataacacaaa actttaacat actttaaca aatcttgatt gaataacaac  
121 agattctaca tgacatttta aatcactaaa actcttttga aatcataaac caataacaac  
181 cccttagttt ttactatttt gaattctgac gtactttttt attagttgaa ttctataaaa  
241 tgagaaaaca ttaattatth cttaatcttt gaacttaagc cccacaaaaa tcttataaat  
10 301 tgggacagat ggactagata acaagcgttt cacctactcc aaaatttccc tataagtaac  
361 tcttttttga acctcctttt cttcccaaac catcactcct ttgcatgtgt gtgaaacctt  
421 cgagtthttt cttcatcttc tcaaagtaac aaactttctc caaacagatt attatataaa  
481 caatctcatc aagaactacg ATGAAATTC CGGCTGTAAA AGTTCCTATT ATCTCTCTC  
541 TCATCACATC TTCTTTGTTC ATACTCTCAA CCGCGGATTC GTgtaagtat acacaatgca  
15 601 ttttcttatt ttagatactt ttctcattag aaatttagct ttcttaataa aattgtattg  
661 tgatgatgga ttaattagCA CCATGCGGAG GAAAATGCAA CGTGAGATGT TCAAAGGCAG  
721 GAAGACAAGA TAGGTGTCTC AAGTATTGTA ATATATGTTG CGAGAAGTGT AACTATTGTG  
781 TTCCTTCAGG CACTTATGGA AACAAAGATG AATGCCCTTG TTACCGCGAT ATGAAGAACT  
841 CCAAAGGCAC GTCCAAATGT CCTTGATcat gttcttaaga ttatccttat agacacaata  
20 901 tcttgaaatg ttaagattgt gcttgatgcc taaaataatg agcttgagat acttctatga  
961 atgaatatgt gaaagatttt gacaataaaa tgatttgatg tattaataa tctttagtga  
1021 agttatatat gtataaatga agtatgaaat atacattgta tgttgcttta catgagaaag  
1081 ataaatctac aacaatccaa tgtatgaaaa ttttactaag ttaactgac agaaacgtta  
1141 attatggttt agaactctgt ggagagatga ttacttttgt aagagaaatt gattgtttgt  
1201 tgtaaatgag gataaagtaa gaagccattt ctcaacacat ggacttgata gcaaaactaaa  
25 1261 caaggctcaa gcattgaaat tgaaaagtct cgatagataa gattggctca agaaaagcaa  
1321 gtgttttttg ttgtagaaaa cagaaattga aattactgtc tacttt

30 MKFPAVKVLIISLLITSSLFILSTA

DSSP

35 CCGKCNVRCSKAGRQDRCLKYCNICCEKCNVCVPSGTYGNKDECPCYRDMKNSKGTSKCP\*

N. At3g10170

genomic structure before splicing and processing 5'- towards 3'  
predicted orf sequences are underlined

5  
10  
15  
20

CTGTTTCAGAAAATGGCAACAAACTTAGCATCATTGTTTCTCCATTG  
TTGTGTTACATCTTCTTCTGTCTGCCCATATGCATGTAAGTGTTCAACA  
CTCTATTCCCTCTATGTTTACATTTATCAACTTTATCTTATACGTCCTGA  
ATAAAACACAGCCTATATACCTGGAACTCCTGCTCGACAACCACAACCA  
CCACAGTCGCAACCACAACCTGCCGCATCACAATAACTCTCAAGTGAGTTT  
CTCGGTTTCATCACTACTCAAAAAAAGAGTTTCATCGAATCTACAAAACCT  
TTTAAACATCCTTTGCATCTTCTGTGATTGTCAGTACGGTACTACT  
CAAGGCAGTCTTCAACCCCAAGGTAAACCCACTGACTAGCCTAGTTTTTA  
ATTAATGTTTGTGCTGAATGCGAACTAAATCCGCTATTCCACCTTTATT  
AGAGTGCGGGCCAAGGTGTGSAGATAGTCTCGAATACACAATACAAGA  
AGCCGTGTTTGTCTTCTGCAACAATGTTGTAACAAGTGCTTGTGTGTG  
CCCCCAGGTACTTATGGCAATAAGCAAGTATGCTTGTCTATAACAACCTG  
GAAGACCAAGAGCGGTGGACCAAAATGCCCTTAGTTTCTCCTCTTAATTA  
CTTTAGCATAAACTCCATGTAATTTGTTAATCTACCTATCATAATTATA  
TATGATTGGACTCTTCCATAATCACATCAGTTCTCTGTGATTATGACGT

25

Amino acid sequence of the predicted pre-pro-peptide  
the first line represents the signal sequence  
the second (set of) lines represents the the pro-peptide  
the last line represents the conserved Cysteine motif.

MATKLSIIVFSIVVLHLLLSAHMH

30

FLINVCAECETKSAIPPLLE

CGPRCGDRCSNTQYKKPCLFFCNKCCNKCLCVPPGTYGNKQVCPYNNWTKSGGPKCP\*

35

They consist of an N-terminal signal peptide, followed by a  
variable domain (involved in mobility or cell wall attachment)  
5 and a C-terminal domain with 12 conserved cystein residues.

The consensus of this last domain is:

C-C-RC-----C---C--CC-(R/K)C-CVP(P/S)GT-G(N/H)---C-CY-----G--KCP\*

(-) = any amino acid;

(C) = conserved C-residue

10 (/) = either one or the other amino acid at this position;

\* = stopcodon

Some members of this gene family have been described  
previously, and represent the GASA family in *Arabidopsis*  
15 *thaliana* (Plant Mol. Biol. 36 (1998). Similar family  
members containing the same structural motifs are present in  
rice (like GASR1) and tomato (Plant Journal 2 (1992) 153-159;  
Mol. Gen. Genet. 243 (1994) Taylor and Scheuring). In  
*Arabidopsis*, the GASA gene family represents 14 different  
20 membres, similar as the number for the RKS gene family. Our  
data on the similar phenotypes for RKS4 and GASA3 (figure 6)  
and the fact that there are similar numbers of ligands and  
receptors suggest that there is a single GASA ligand molecule  
interaction with a single RKS molecule. T-DNA knock out  
25 phenotypes observed with several of the other GASA peptide  
ligand genes also show modifications of organ and plant size  
like the appearance of extreme dwarf plants resembling  
brassinosteroid insensitive mutants. Co-localization of RKS  
genes and GASA ligands on the genome (see figure 4) could  
30 provide clues of molecular interactions between GASA molecules  
and RKS molecules (similar as for S locus proteins and S locus  
receptor kinases).

Furthermore, in the chapter discussing the effects of roots in  
RKS transgenic plants, it was shown that overexpression of RKS  
35 genes can result in the formation of lateral roots (figure  
26). One of the GASA ligands is involved in the formation  
and/or outgrowth of lateral roots as discussed in Mol. Gen.  
Genet. 243, 1994, 148-157.

Intracellularly, this signal is transmitted onto membrane (but not necessarily plasma membrane) associated NDR-NHL proteins. At least some of the functions of the syntaxin-like NDR-NHL

5 proteins would thereby result in the regulation of vesicle transport and /or the positioning of new cell wall formation. Neighboring cells are known to influence and determine the developmental state and the differentiation of cells. In transgenic plants with RKS and / or NDR-NHL expression

10 cassettes the positioning of new cell walls is modified, resulting in abnormal neighboring cells, resulting in abnormal development of groups of cells like flower meristem primordia as observed and shown with RKS0, RKS13 and NHL10.

Table 2 overview of accessions numbers of RKS signal complex genes in arabidopsis and in rice:

Gene code	contig	gene prediction in At database	Oryza sativa japonica contig	approximate position in bp around:
RKS0 At1g71830	f14c23	ok	OSJNBa0036B21	52.000
RKS1 At1g60800	f8a5	ok	P0038C05	60.000
RKS2 At5g65240	mgn23	ok	OJ1212_C08	8000
RKS3 At5g63710	mbk5	ok	see rks2	
RKS4 At2g23950	t29e15	wrong, exon missing	P0708B04	35.000
RKS5 At5g45780	mra19	wrong, exon missing	OJ1077_A12	102.000
RKS6 At5g10290	wt e 23	ok	see rks2	
RKS7 At5g16000	ku e 24	ok	P0038C05	60.000
RKS8 At1g34210	f23ml9	ok	OJ1134_B10	90.000 & 1000 2
15 different genes!				
RKS10 At4g33430	en d 25	wrong, exon missing	see rks0	
RKS11 At4g30520	wu d 20	wrong, exon missing	see rks4	
RKS12 At2g13800	f13jl1	wrong, exon missing	see rks10	
RKS13 At2g13790	f13jl1	ok	P0633E08	36.000
RKS14 At3g25560	mw12	wrong, exon missing	OSJNBb0015G09	36.000
ELS1 At5g21090	ch e 52	ok	P0003H10	53.000
ELS2 possibly allelic variant of ELS1 no genomic sequence identified yet				see els1
ELS3 At3g43740	by c 21	ok	P0468B07	52.000

Homology between aa sequences from arabidopsis proteins are compared with the rice databases using:  
[http://mips.gsf.de/proj/thal/db/search/search\\_frame.html](http://mips.gsf.de/proj/thal/db/search/search_frame.html)  
 protein sequences based on *Oryza sativa japonica* contig sequences.

*Arabidopsis thaliana* ELS1 cDNA

The start codon encoding the first predicted methionine  
5 residue of the gene product has been indicated by bold  
capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in  
capitals. Leader and trailer sequences are in lowercase  
10 letters.

```
ttactctcaaattccttttcgatttcctctcttaaacctccgaaagctcac
ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAACCCCTAA
CCTTAGCTTTGATTACCTGGTCGAAGCAAACCTCCGAAGGAGATGCTCTCTA
15 CGCTCTTCGCCGGAGTTTGACAGATCCAGACCATGTCTCCAGAGCTGGGAT
CCAACTCTTGTTAATCCTGTACCTGGTTCCATGTCACCTGTAACCAAGACA
ACCGCGTCACTCGTGTGGATTGGGAAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTACAGTATCTAGAGCTCTACAAAAC
AACATCCAAGGAATAACCTTCCGAACTTGGAAATCTGAAGAATCTCATCA
20 GCTTGGATCTGTACAACAACATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACGGTC
CAATCCCTAGAGCACTCACGGCAATCCCAAGCCTTTAAAGTTGTGACGTCTC
AAGCAATGATTTGTGTGGACAATCCACAAACGGACCCTTTGCTCACATTCC
TTTACAGAACTTTGAGAACAACCCGAGATTGGAGGGACCGGAATTACTCGGT
25 CTTGCAAGCTACGACACTAACTGCACCTGAaacaactggcaaacctgaaaat
gaagaattgggggtgaccttgaagaacacttcaccactttatcaaatatc
acatctactatgtaataagtatatatatgtagtccaaaaaaaaaaaaaaaaa
```

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS1  
30 protein.

Different domains are spaced and shown from the N-terminus  
towards the C-terminus. Overall domain structure is similar as  
described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain  
35 represents a signal sequence. The second domain contains a  
leucine zipper motif, containing 4 leucine residues, each  
separated by seven other amino acids. The third domain  
contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

5

MASRNYRWELFAASL  
TLTLALIHLEVEANSEG

DALYALRRSLTDP

10 DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

DLGNSNLSGHLA

15 P ELGKLEHLQYLELYKNNIQGTI  
PSELGNLKNLISLDLYNNNLTGIV  
PTSLGKLKSLVFLRLNDNRLTGPI  
PRALTAIPSLKVVDVSSNDLCGTI  
PTNGPFAHIPLQNFENNPRLEGPE

20

LLGLASYDTNCT

*Arabidopsis thaliana* ELS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 aaaattactcaaattcctattagattactctcttcgacctccgatagctcac  
 ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAATCCTAA  
 CCTTAGCTTTGATTACCTGGTCGAAGCAAACCTCCGAAGGAGATGCTCTTTA  
 CGCTCTTCGCCGGAGTTTAAACAGATCCGGACCATGTCTCCAGAGCTGGGAT  
 CCAACTCTTGTTAATCCTTGTTACCTGGTCCATGTACCTGTAACCAAGACA  
 15 ACCGCGTCACTCGTGTGGATTGGGGAATCAAACCTCTCTGGACATCTTGC  
 GCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAC  
 AACATCCAAGGAACATACCTTCCGAACCTGGAAATCTGAAGAATCTCATCA  
 GCTTGGATCTGTACAACAACAATCTTACAGGGATAGTTCCCACTTCTTTGGG  
 AAAATTGAAGTCTCTGGTCTTTTACGGCTTAATGACAACCGATTGACGGGG  
 20 CAATCCCTAGAGCACTCACTGCCAATCCCAAGCCTTAAAAGTTGTGGATGTC  
 TAAGCAATGATTTGTGTGGAACAATCCCAACAAACGGACCTTTTGCTCACAT  
 TCCTTTACAGAACCTTTGAGAACAACCCGAGGTTGGAGGGACCGGAATTACTC  
 GGTCTTGCAAGCTACGACACTAACTGCACCTGAagaaattggcaaaacctga  
 aaatgaagaattgggggggaccttgtaagaacacttcaccactttatcaa  
 25 atcacatctactatgtaataagtatatatatgtagtccaaaaaaaaaatgaa  
 gaatcgaatagtaatatcatctggtctcaattgagaactttgaggtctgtgt  
 atgaaaattaaagattgtactgtaatgttcggttggtgattctgagaagta  
 acatttgattgggtatggtatcaagttgttctgccttgctgcaaaaaaaaa

30

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as  
 35 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain

contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be  
5 involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELFAASL  
ILTLALIHLEVEANSEG

10

DALYALRRSLTDP  
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

15

DLGNSNLSGHLA

P ELGKLEHLQYLQLYKNNIQGTI  
PSELGNLKNLISLDLYNNNLTGIV  
PTSLGKLKSLVFLRLNDNRLTGPI  
20 PRALTAIPSLKVVDVSSNDLCGTI  
PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT

25

*Arabidopsis thaliana* ELS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttctctctccggcgaaaacc**ATGGTGGCGCAAACAGTCGGCGGGAGCTTCTAGCAGCTT**  
 CCCTGATCCTAACTTTAGCTCTAATTCGTCTAACGGAAGCAAAC**TCCGAAGGGGACGCTC**  
 TTCACGCGCTTCGCCGGAGCTTATCAGATCCAGACAATGTTGTT**CAGAGTTGGGATCCAA**  
 CTCTTGTTAATCCTTGTA**CTTGGTTTCATGTCACTTGTAATCAACACCATCAAGTCACTC**  
 GTCTGGATTGGGGAATTCAACTTATCTGGACATCTAGTACCTGA**ACTTGGGAAGCTTG**  
 15 AACATTTACAATATCTTGA**ACTCTACAAAACGAGATTCAAGGA**ACTATACCTTCTGAGC  
 TTGGAAATCTGAAGAGTCTAATCAGTTTGGATCTGTACAACA**CAATCTCACC**GGGAAAA  
 TCCCATCTTCTTTGGGAAATGAAGCGGCTTAACGAA**ACCGATTGACCGGTCCTATTC**  
 CTAGAGAACTCACAGTTATTTCAAGCCTTAAAGTTGTTGATGTCTCAGGGAATGATTTGT  
 GTGGAA**CAATCCAGTAGAAGGACCTTTTGAACACATTCC**TATGCAAACTTTGAGAACA  
 20 ACCTGAGATTGGAGGGACCAGAACTACTAGGTCTTGC**GAGCTATGACACCAATTGCACTT**  
AAaaagaagttgaagaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS3 protein.

25 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a

30 leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each  
 35 approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MVAQNSRRELLAASL  
ILTLALIRLTEANSEG

5 DALHALRRSLSDP  
DNVVQSWDPTLVN

PCTWFHVTCNQHHQVTRL

DLGNSNLSGHLV  
10 P ELGKLEHLQYLELYKNEIQGTI  
PSELGNLKSLSLDLYNNNLTGKI  
P SSLGKLKRLNENRLTGPI  
PRELTVISSLKVVDVSGNDLCGTI  
PVEGPFHEIPMQNFENNLRLLEGPE  
15 LLGLASYDTNCT

*Arabidopsis thaliana* RKS0 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atttttatttttattttttactctttgtttgttttaatgctaattgggtttttaaaagggtt  
atcgaaaaaatgagtgagtttggttgaggttgctctgttaaagtgttaatggtggtgat  
tttcggaagtttagggttttctcgatctgaagagatcaaatcaagattcgaaatttacca  
ttgttggttgaa**ATGGAGTCGAGTTATGTGGTGT**TTATCTTACTTTCACTGATCTTACTT  
CCGAATCATTCACTGTGGCTTGCTTCTGCTAATTTGGAAGGTGATGCTTTCATACTTTG  
15 AGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAAGAGCTGGGATCCTACGCTAGTGAAT  
CCTTGACATGGTTCCATGTCATTGCAACAACGAGAACAGTGTCTAAGAGTTGATTTG  
GGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAG  
TATTTGGAGCTTTACAGTAACAACATAACTGGCCCGATTCTAGTAATCTTGGAAATCTG  
ACAAACTTAGTGAGTTTGGATCTTTACTTAAACAGCTTCTCCGGTCTATTCCGGAATCA  
20 TTGGGAAAGCTTTCAAAGCTGAGATTTCTCCGGCTTAACAACAACAGTCTCACTGGGTCA  
ATTCTATGTCACTGACCAATATTACTACCCTTCAAGTGTTAGATCTATCAAATAACAGA  
CTCTCTGGTTCAGTTCCTGACAATGGCTCCTTCTCACTCTTCACACCCATCAGTTTGTCT  
AATAACTTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCTGGATCTCCCCGTTT  
TCTCTCCACCACCTTTTATTCAACCTCCCCAGTTTCCACCCGAGTGGGTATGGTATA  
25 ACTGGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTTGCCCTTTGCTGCTCTGCA  
ATAGCCTTTGCTTGGTGGCGACGAAGAAGCCCACTAGATATTTCTTCGATGTCCCTGCC  
GAAGAAGATCCAGAAGTTCATCTGGGACAGCTCAAGAGGTTTCTTTGCGGGAGCTACAA  
GTGGCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGAAAGTC  
TACAAGGGACGCTTGGCAGACGGAACCTTGTGCTGTCAAGAGACTGAAGGAAGAGCGA  
30 ACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCAT  
CGAAACCTGTTGAGATTACGAGGTTTCTGTATGACACCGACCGAGAGATTGCTTGTGTAT  
CCTTACATGGCCAATGGAAGTGTGCTTCGTGTCTCAGAGAGAGGCCACCGTCACAACCT  
CCGCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGGCTCAGCTCGAGGTTTGTCTTAC  
CTACATGATCACTGCGATCCGAAGATCATTCACCGTGACGTAAAAGCAGCAAACATCCTC  
35 TTAGACGAAGAATTCTGAAGCGGTTGTTGGAGATTTGCGGTTGGCAAAGCTTATGGACTAT  
AAAGACACTCACGTGACAACAGCAGTCCGTGGCACCATCGGTCACATCGCTCCAGAATAT  
CTCTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTTTCGGATACGGAATCATGCTTCTA  
GAACTAATCACAGGACAAAGAGCTTTCGATCTCGCTCGGCTAGCTAACGACGACGACGTC  
ATGTTACTTGAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGAT  
40 CCAGATCTTCAAACAACTACGAGGAGAGAGAACTGGAACAAGTGATACAAGTGGCGTTG

CTATGCACGCAAGGATCACCAATGGAAAGACCAAAGATGTCTGAAGTTGTAAGGATGCTG  
GAAGGAGATGGGCTTGCGGAGAAATGGGACGAATGGCAAAAAGTTGAGATTTGAGGGAA  
GAGATTGATTTGAGTCCTAATCCTAACTCTGATTGGATTCTTGATTCTACTTACAATTTG  
CACGCCGTTGAGTTATCTGGTCCAAGGTAAaaaaaaaaaaaaaaaaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS0 protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a  
signal sequence. The second domain contains a leucine zipper motif,  
containing 4 leucine residues, each separated by seven other amino  
15 acids. The third domain contains conserved cysteine residues,  
involved in disulphate bridge formation. The fourth domain contains a  
leucine rich repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain contains many  
serine and proline residues, and is likely to contain hydroxy-proline  
20 residues, and to be a site for O-glycosylation. The sixth domain  
contains a single transmembrane domain after which the predicted  
intracellular domains are positioned. The seventh domain has an  
unknown function. The eight domain represents a serine / threonine  
protein kinase domain (Schmidt et al. 1997) and is probably also  
25 containing sequences for protein / protein interactions. The ninth  
domain has an unknown function. The last and tenth domain at the C-  
terminal end represents part of a single leucine rich repeat,  
probably involved in protein / protein interactions.

30

MESSYVVFILLSLILLPNHSL  
WLASANLEG

DALHTLRVTLVDP

35

NNVLQSWDPTLVN

PCTWEHVTCNNENSVIRV

DLGNAELSGHLV

40

P ELGVLKNLQYLELYSNNITGPI

PSNLGNLTNLVSLDLYLNSFSGPI  
PESLGKLSKLRFLRLNNSLTGSI  
PMSLTNITTTLQVLDLSNNRLSGSV  
PDNGSFSLFTPISFANNLDLCGPV

5

TSHPCPGSPPFSPPPP  
FIQPPPVSTPSGYGITG

AIAGGVAAGAAL  
10 PFAAPAIAFWW

RRRKPLDIFFDVPAEEDPE  
VHLGQLKRFSLRELQVAS

15 DGFSNKNILGRGGFGKVYKGRAD  
GTLVAVKRLKEERTPGGELQFQ  
TEVEMISMAVHRNLLRLRGFCM  
TPTERLLVYPYMANGSVASCLR  
ERPPSQPPLDWPTRKRIALGSA

20 RGLSYLHDHCDPKIIHRDVKAA  
NILLDEEFEAVVGDFGLAKLMD  
YKDTHTVTAVRGITIGHIAPEYL  
STGKSSEKTDVFGYGIMLLELI  
TGQRAFDLARLANDDDVMLLDW

25 VKGLLKEKKLEMLVDPDLQTNV  
EERELEQVIQVALLCTQGSPME  
RPKMSEVVRMLE

GDGLAEKWDEWQKVEILREEIDLS  
30 PNPNSDWILDSTYNLHVELSGPR

*Arabidopsis thaliana* RKS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ccaaagttgattgctttaagaagggat**ATGGAAGGTGTGAGATT**TGTGGTGTGGAGATTA  
GGATTCTGGTTTTTGTATGGTTCTTTGATATCTTCTGCTACACTTTCTCCTACTGGT  
GTAACATATGAAGTGACAGCTTTGGTTGCTGTGAAGAATGAATTGAATGATCCGTACAAA  
GTTCTTGAGAATTGGGATGTGAATCAGTTGATCCTTGTAGCTGGAGAATGGTTTCTTGC  
ACTGATGGCTATGTCTCTTCACTGGATCTTCCTAGCCAAAGCTTGCTGGTACATTGTCT  
15 CCTAGAATCGGAAACCTCACCTATTTACAATCAGTGGTGTGCAAAACAATGCAATCACT  
GGTCCAATTCGGGAAACGATTGGGAGGTTGGAGAAGCTTCAGTCACCTTGATCTTTCGAAC  
AATTCATTACCGGGGAGATACCGGCCTCACTTGGAAGCAAGAACTTGAATTACTTG  
CGTTAAACAATAACAGTCTTATAGGAACCTTGCCCTGAGTCTCTATCCAAGATTGAGGGA  
CTCACTCTAGTCGACATTTTCGTATAACAATCTTAGTGGTTCGCTGCCAAAAGTTTCTGCC  
20 AGAAGCTTTCAAGGTAATTGGTAATGCGTTAATCTGTGGCCCAAAGCTGTTTCAAAGTGT  
TCTGCTGTTCCCGAGCCTCTCACGCTTCACAAGATGGTCCAGATGAATCAGGAACTCGT  
ACCAATGGCCATCACGTTGCTCTTGCATTTGCCGCAAGCTTCAGTGCAGCATTTTTTGT  
TTCTTTACAAGCGGAATGTTTCTTTGGTGGAGATATCGCCGTAACAAGCAAATATTTTTT  
GACGTTAATGAACAATATGATCCAGAAGTGAGTTTAGGGCACTTGAAGAGGTATACATTC  
25 AAAGAGCTTAGATCTGCCACCAATCATTTCAACTCGAAGAACATTCTCGGAAGAGGCGGA  
TACGGGATTGTGTACAAAGGACACTTAAACGATGGAACCTTTGGTGGCTGTCAAACGTCTC  
AAGGACTGTAACATTGCGGGTGGAGAAGTCCAGTTTCAGACAGAAGTAGAGACTATAAGT  
TTGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACCAGGAGAGA  
ATTTTAGTCTACCTTACATGCCAAATGGGAGTGTGCGATCACGCTTAAAGATAATATC  
30 CGTGGAGAGCCAGCATTAGACTGGTCGAGAAGGAAGAAGATAGCGGTTGGGACAGCGAGA  
GGACTAGTTTACCTACACGAGCAATGTGACCCGAAGATTATACACCGCGATGTGAAAGCA  
GCTAACATTCTGTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTTTGGGTTAGCTAAG  
CTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAAGTGTGGCCACATT  
GCACCTGAGTACTTATCCACGGGTCAGTCTCAGAGAAGACTGATGTCTTTGGCTTTGGC  
35 ATACTTCTCCTTGAGCTCATTACTGGTCAGAAAGCTCTTGATTTTGGCAGATCCGCACAC  
CAGAAAGGTGTAATGCTTGACTGGGTGAAGAAGCTGCACCAAGAAGGGAACATAAGCAG  
TTAATAGACAAAGATCTAAATGACAAGTTCGATAGAGTAGAACTCGAAGAAATCGTTCAA  
GTTGCGCTACTCTGCACTCAATTCAATCCATCTCATCGACCGAAAATGTCAGAAGTTATG  
AAGATGCTTGAAGGTGACGGTTTGGCTGAGAGATGGGAAGCGACGCAGAACGGTACTGGT  
40 GAGCATCAGCCACCGCCATTGCCACCGGGATGGTGAGTTCTTCGCCGCTGTGAGGTAT

TACTCGGATTATATTCAGGAATCGTCTCTTGTAGTAGAAGCCATTGAGCTCTCGGGTCCT  
CGATGAttatgactcactgtttttaaaaaa

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate  
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-  
20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably  
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MEGVRFVVWRLGFL  
VFVWFFDISSATLSPTGVNYEV

TALVAVKNEINDP

35 YKVLNWDVNSVD

PCSWRMVSCDGYVSSL

DLPSQSLSGT  
LSPRIGNLTYLQSVLQNNAITGPI  
PETIGRLEKLQSLDLSNNSFTGEI  
PASLGELKNLNYLRNLNNSLIGTC  
5 PESLSKIEGLTLVDISYNNLSGSL  
PKVSARTFK VIGNALICGPK  
  
AVSNCSAVPEPLTL  
PQDGPDESGTRTNG  
10  
HHVALAFAASFS  
AAFFVFFFTSGMFLWW  
  
RYRRNKQIFFDVNEQYDPE  
15 VSLGHLKRYTFKELRSAT  
  
NHFNSKNILGRGGYGIVYKGHLND  
GTLVAVKRLKDCNIAGGEVQFQ  
TEVETISLALHRNLLRLRGFCS  
20 SNQERILVYPMPNGSVASRLK  
DNIRGEPALDWSRRKKIAVGTA  
RGLVYLHEQCDPKIIHRDVKAA  
NILDEDFEAVVGDFGLAKLLD  
HRDSHVTTAVRGTVGHIAPEYL  
25 STGQSSEKTDVFGFGILLLELI  
TGQKALDFGRSAHQKGVMLDW  
VKKLHQEGKLKQLIDKDLNDKF  
DRVELEEIVQALLCTQFNPSH  
RPKMSEVMKMLE  
30  
GDGLAERWEATQNGTGEHQPPPLPPGMVSSS  
  
PRVRYSDYIQESSLVVEAIELSGPR  
35

*Arabidopsis thaliana* RKS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

Italics indicate the presence of an alternatively spliced gene product.

10

tcaat<sup>ttt</sup>tgtagctccttagaaaa**ATGGCTCTGCTTATTATCACTGCCTTAGT**TTTTAGT  
AGTTTATGGTCATCTGTGTACCAGATGCTCAAGGGGATGCATTATTTGCGTTGAGGAGC  
TCGTTACGTGCATCTCCTGAACAGCTTAGTGATTGGAACCAGAATCAAGTCGATCCTTGT  
ACTTGGTCTCAAGTTATTTGTGATGACAAGAAACATGTTACTTCTGTAACCTTGTCTTAC

15

ATGAACCTCTCCTCGGGAACACTGTCTTCAGGAATAGGAATCTTGACAACTCTCAAGACT  
CTTACATTGAAGGGAAATGGAATAATGGGTGGAATACCAGAATCCATTGGAAATCTGTCT  
AGCTTGACCAGCTTAGATTTGGAGGATAATCACTTAACTGATCGCATTCATCCACTCTC  
GGTAATCTCAAGAATCTACAGTTCTTCAGGACCTTGAGTAGGAATAACCTTAATGGTTCT  
ATCCCGGATTCACTTACAGGTCTATCAAACTGATAAATATTCTGCTCGACTCAAATAAT

20

CTCAGTGGTGAGATTCTCAGAGTTTATTCAAAATCCCAAATACAATTCACAGCAAAC  
AACTTGAGCTGTGGTGGCACTTTCCCGCAACCTTGTAACCGAGTCCAGTCCTTCAGGT  
GATTCAAGCAGTAGAAAACTGGAATCATCGCTGGAGTTGTTAGCGGAATAGCGGTTATT  
CTACTAGGATTCTTCTTCTTTTCTTCTGCAAGGATAAACATAAAGGATATAAACGAGAC  
GTATTTGTGGATGTTGCAGGAACGAACCTTAAAAAAGGTTTGATTTCAAGGTGAAGTGGAC

25

AGAAGGATTGCTTTTGGACAGTTGAGAAGATTGTCATGGAGAGAGCTTCAGTTGGCTACA  
GATGAGTTCAAGTGAAGAAGATGTTCTCGGACAAGGAGGCTTTGGGAAAGTTTACAAAGGA  
TTGCTTTTCGGATGGCACCAGTTCGCTGTAAAAAGATTGACTGATTTTGAACGTCCAGGA  
GGAGATGAAGCTTTCCAGAGAGAAGTTGAGATGATAAGTGTAGCTGTTTCATAGGAATCTG  
CTTCGCCTTATCGGCTTTTGTACACACAACTGAACGACTTTTGGTGTATCCTTTCATG

30

CAGAATCTAAGTGTTCATATTGCTTAAGAGAGATTAAACCCGGGGATCCAGTTCTGGAT  
TGGTTCAAGGAGAAACAGATTGCGTTAGGTGCAGCACGAGGACTCGAATATCTTCATGAA  
CATTGCAACCCGAAGATCATACACAGAGATGTGAAAGCTGCAATGTGTTACTAGATGAA  
GACTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAGTTGGTAGATGTTAGAAGGACT  
AATGTAACCACTCAGGTCCGAGGAACAATGGGTCATATTGCACCAGAATGTATATCCACA

35

GGGAAATCGTCAGAGAAAACCGATGTTTTCGGGTACGGAATTATGCTTCTGGAGCTTGT  
ACTGGACAAAGAGCAATTGATTTCTCGCGTTAGAGGAAGAAGATGATGCTTATTGCTA  
GACCATGTGAAGAACTGGAAAGAGAGAAGAGATTAGAAGACATAGTAGATAAGAAGCTT  
GATGAGGATTATATAAAGGAAGAAGTTGAAATGATGATACAAGTAGCTCTGCTATGCACA  
CAAGCAGCACCGGAAGAACCAGACGCGATGTCGGAAGTAGTAAGAATGCTAGAAGGAGAA

40

GGGCTTGCAGAGAGATGGGAAGAGTGGCAGAATCTTGAAGTGACGAGACAAGAAGAGTTT

CAGAGGTTGCAGAGGAGATTGATTGGGGTGAAGATTCCATTAATAATCAAGATGCTATT  
GAATTATCTGGTGAAGATAGaaacaaaaaa

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS2 protein.
- Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
- 15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 3 complete and 2 incomplete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site
- 20 for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
- 25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions. Italics indicate an alternatively spliced gene
- 30 product.

MALLIITALVFSSL  
WSSVSPDAQG

35 DALFALRSSLR  
ASPEQLSDWNQNQVD

PCTWSQVICDDKKHVTSV

T L S Y M N F S S   G T L S S G I  
G     I L T T L K T L T L K G N G I M G G I  
P E S I G N L S S L T S L D L E D N H L T D R I  
5   P S T L G N L K N L Q F L T L S R N N L N G S I  
     P D S L T G L S K L I N I L L D S N N L S G E I  
     P Q S L F K I P K Y N   F T A N N L S C G G  
  
T F P Q P C V T E S S P S G D S S S R K T G  
10  
     I I A G V V S G I A V I L  
     L G F F F F F F C  
  
K D K H K G Y K R D V F V D V A G T N F K K G L I S G E  
15   V D R R I A F G Q L R R F A W R E L Q L A T  
  
D E F S E K N V L G Q G G F G K V Y K G L L S D  
G T K V A V K R L T D F E R P G G D E A F Q  
R E V E M I S V A V H R N L L R L I G F C T  
20   T Q T E R L L V Y P F M Q N L S V A Y C L R  
     E I K P G D P V L D W F R R K Q I A L G A A  
     R G L E Y L H E H C N P K I I H R D V K A A  
     N V L L D E D F E A V V G D F G L A K L V D  
     V R R T N V T T Q V R G T M G H I A P E C I  
25   S T G K S S E K T D V F G Y G I M L L E L V  
     T G Q R A I D F S R L E E D D V L L L D H  
     V K K L E R E K R L E D I V D K K L D E D Y  
     I K E E V E M M I Q V A L L C T Q A A P E E  
     R P A M S E V V R M L E  
30  
     G E G L A E R W E E W Q N L E V T R Q E E F Q  
  
R L Q R R F D W G E D S I N N Q D A I E L S G G R  
35

*Arabidopsis thaliana* RKS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

aacggtgaaagtttccatgatcctcttcgaggattcattcaaagaaattgcttttagatgg  
10 aacaatcagaaattgatcttacaatgtttc**ATGGCCTTAGCTTTGTGGGAATCACTTCG**  
TCAACA**ACTCAACCAGATATCGAAGGAGGAGCTCTGTGCAGCTCAGAGATTCGCTTAAT**  
GATTCGAGCAATCGTCTAA**AATGGACACGCGATTTTGTGAGCCCTTGCTATAGTTGGTCT**  
TATGTTACCTGCAGAGGCCAGAGTGT**TGTGGCTCTAAATCTTGCTCGAGTGGATTCA**  
GGAACACTCTCTCCAGCTATTACAA**ACTGAAGTTCTTGGTTACCTTAGAGTTACAGAAC**  
15 AATAGTTTATCTGGTGCTTACCAGATTCTCTTGGGAACATGGTTAATCTACAGACTT**A**  
AACCTATCAGTGAATAGTTT**CAGCGGATCGATACCAGCGAGCTGGAGTCAGCTCTCGAAT**  
CTAAAGCACTTGGATCTCTCATCCAATAATTTAACAGGAAGCATCCCAACACAATTCTTC  
TCAATCCCAACATTCGATTTT**CAGGA**ACTCAGCTTATATGCGGTAAAAGTTTGAATCAG  
CCTTGTCTCTCAAGTTCTCGTCTTCCAGTCACATCCTCCAAGAAAAGCTGAGAGACATT  
20 ACTTTGACTGCAAGTTGTGTGCTTCTATAATCTTATTCCTTGGAGCAATGGTTATGTAT  
CATCACCATCGCGTCCGCAGAACCAATACGACATCTTTTTT**GATGTAGCTGGGGAAGAT**  
GACAGGAAGATTTCTTTGGACA**ACTAAAACGATTCTCTTTACGTGAAATCCAGCTCGCA**  
ACAGATAGTTTCAACGAGAGCAATTTGATAGGACAAGGAGGATTTGGTAAAGTATACAGA  
GGTTTGCTTCCAGACAAAACAAAAGTTGCAGTGAAACGCCTTGCGGATTACTTCAGTCCT  
25 GGAGGAGAAGCTGCTTTCCAAAGAGAGATT**CAGCTCATAAGCGTTGCGGTTCA**AAAAAT  
CTCTTACGCCTTATTGGCTTCTGCACA**ACTTCCTCTGAGAGAATCCTTGTTATCCATAC**  
ATGGAAAATCTTAGTGTTGCATATCGACTAAGAGATTTGAAAGCGGGAGAGGAAGGATTA  
GACTGGCCAACAAGGAAGCGTGTAGCTTTTGGTTCAGCTCACGGTTTAGAGTATCTACAC  
GAACATTGTAAACCGAAGATCATACACCGCATCTCAAGGCTGCAAACATACTTTTAGAC  
30 AACAAATTTGAGCCAGTTCTTGGAGATTTCGGTTTAGCTAAGCTTGTGGACACATCTCTG  
ACTCATGTCACACTCAAGTCCGAGGCACAATGGGTCACATTGCGCCAGAGTATCTCTGC  
ACAGGAAAATCATCTGAAAAAACCGATGTTTTTGGTTACGGTATAACGCTTCTTGAGCTT  
GTTACTGGTCAGCGCGCAATCGATTTTTCACGCTTGAAGAAGAGGAAAATATTCTCTTG  
CTTGATCATATAAAGAAGTTGCTTAGAGAACAGAGACTTAGAGACATTGTTGATAGCAAT  
35 TTGACTACATATGACTCCAAAGAAGTTGAAACAATCGTTCAAGTGGCTCTTCTCTGCACA  
CAAGGCTCACCAGAAGATAGACCAGCGATGTCTGAAGTGGTCAAAATGCTTCAAGGGACT  
GGTGGTTTGGCTGAGAAATGGACTGAATGGGAACA**ACTTGAAGAAGTTAGGAACAAAGAA**  
GCATTGTGCTTCCGACTTACCGGCTACTTGGGATGAAGAAGAAACCACCGTTGATCAA  
GAATCTATCCGATTATCGACAGCAAGATGAagaagaacagagagagaaagatatctatg  
40 aaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS3 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a  
10 leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 4 complete repeats of each  
15 approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular  
20 domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth  
25 domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MALAFVGITSSSTQPDIEG

30

GALLQLRDSLNDSSNRL

KWTRDFVS

PCYSWSYVTCRGQSVVAL

35

NLASSGFTGTLS

P AITKLKFLVTLELQNNLSLGGAL

PDSLGNMNVNLQTLNLSVNSFSGSI

PASWSQLSNLKHLDLSSNNLTGSI  
PTQFFSIPTFEFSGTQLICGKS

5 LNQPCSSSRPVTSSKKKLRD

ITLTASCVASIIL  
FLGAMVMYHHH

10

RVRRTKYDIFFDVAGEDDR  
KISFGQLKRFSLEIQLAT

DSFNESNLIGQGGFGKVYRGLLPD

15 KTKVAVKRLADYFSPGGEAAFQ  
REIQLISVAVHKNLLRLIGFCT  
TSSEIRLVYPYMENLSVAYRLR  
DLKAGEEGLDWPTRKRVAFGSA  
HGLEYLHEHCNPKIIHRDLKAA

20 NILLDNNFEPVLGDFGLAKLVD  
TSLTHVTTQVRGTMGHIAPEYL  
CTGKSSEKTDVFGYGITLLELV  
TGQRAIDFSRLEEEENILLLD  
HIKKLLREQRLROIVDSNLTTY

25 DSKEVETIVQVALLCTQGSPED  
RPAMSEVVKMLQ

GTGGLAEKWTEWEQLEEVNRKEALLL

30 PTLPATWDEEETTVDQESIRLSTAR

*Arabidopsis thaliana* RKS4 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tcttccttctccttctcgtaatctaataagcttttc**ATGGTGGT**GATGAAGATATTC  
TCTGTTCTGTTACTACTATGTTTCTTCGTTACTTGTCTCTCTTCTGAACCCAGAAAC  
CCTGAAGTGGAGGCGTTGATAAACATAAAGAACGAGTTACATGATCCACATGGTGTTC  
AAAACTGGGATGAGTTTCTGTGATCCTGTAGCTGGACTATGATCTCTGTTCTTCA  
GACAACCTCGTAATTGGCTTAGGAGCTCCAAGTCAGTCTCTTCAGGAACTTATCTGGG  
15 TCTATTGGAAATCTCACTAATCTTCGACAAGTGTCAATACAGAAACAATAACATCTCCGGT  
AAAATCCCAACCGAGATTTGTCTCTTCCCAAATTACAGACTCTGGATTTATCCAATAAC  
CGGTTCTCCGGTGAAATCCCCGGTCTGTTAACCAGCTGAGTAATCTCCAATATCTGTTG  
AACAACAACCTCATTATCTGGGCCCTTTCCTGCTTCTGTCTCAAATCCCTCACCTCTCT  
TTCTTAGACTTGCTTATAACAATCTCAGAGGTCCTGTTCCATAAATTCCTGCAAGGACA  
20 TTCAATGTTGCTGGGAACCCTTGATTTGTAAAAACAGCCTACCGGAGATTTGTTCCAGGA  
TCAATCAGTGCAAGCCCTCTTCTGTCTCTTTACGTTCTTCATCAGGACGTAGAACCAAC  
ATATTAGCAGTTGCACTTGGTGTAAGCCTTGGCTTTGCTGTTAGTGTAATCCTCTCTCTC  
GGGTTCAATTGGTATCGAAAGAAACAAGACGGTTAACGATGCTTCGCATTAAACAAGCAA  
GAGGAAGGGTTACTTGGGTTGGGAAATCTAAGAAGCTTCACATTGAGGAACTTCATGTA  
25 GCTACGGATGGTTTTAGTTCCAAGAGTATTCTTGGTGCTGGTGGGTTTGGTAATGTCTAC  
AGAGGAAAATTCGGGGATGGGACAGTGGTTGCAGTGAAACGATTGAAAGATGTGAATGGA  
ACCTCCGGGAACCTCACAGTTTCGTACTGAGCTTGAGATGATCAGCTTAGCTGTTTCATAGG  
AATTTGCTTCGGTTAATCGGTTATTGTGCGAGTTCTAGCGAAAGACTTCTTGTTTACCTT  
TACATGTCCAATGGCAGCGTCGCCTCTAGGCTCAAAGCTAAGCCAGCGTTGGACTGGAAC  
30 ACAAGGAAGAAGATAGCGATTGGAGCTGCAAGAGGGTTGTTTTATCTACACGAGCAATGC  
GATCCCAAGATTATTCACCGAGATGTCAAGGCAGCAAACATTCTCCTAGATGAGTATTTT  
GAAGCAGTTGTTGGGGATTTTGGACTAGCAAAGCTACTCAACCACGAGGATTCACATGTC  
ACRACCGCGGTTAGAGGAACTGTTGGTCACATTGCACCTGAGTATCTCTCCACCGGTCAG  
TCATCTGAGAAAACCGATGTCTTTGGGTTCCGTATACTTTTGCTAGAGCTCATCACAGGA  
35 ATGAGAGCTCTCGAGTTTGCCAAGTCTGTTAGCCAGAAAGGAGCTATGCTAGAATGGGTG  
AGGAAGCTACACAAGGAAATGAAAGTAGAGGAGCTAGTAGACCGAGAACTGGGGACAACC  
TACGATAGAATAGAAGTTGGAGAGATGCTACAAGTGGCACTGCTCTGCACTCAGTTTCTT  
CCAGCTCACAGACCCAAAATGTCTGAAGTAGTTCAGATGCTTGAAGGAGATGGATTAGCT  
GAGAGATGGGCTGCTTCACATGACCATTACATTTCTACCATGCCAACATGTCTTACAGG  
40 ACTATTACCTCTACTGATGGCAACAACCAACCAACATCTGTTTGGCTCCTCAGGATTT

GAAGATGAAGATGATAATCAAGCGTTAGATTCATTCGCCATGGAACATCTGGTCCAAGG  
TAGtaaatcttgacacagaaagaacagatataatatcccatgacttcaatttttgtt

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS4 protein.
- Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
- 15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
- 20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
- 25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.
- 30
- MVVMKLITMKIFSLLLLL  
CFFVTCSLSSEPRNPEV
- EALINIKNELHDP
- 35 HGVFKNWDEFSD
- PCSWTMISCSSDNLVIGL

GAPSQLSGTLS  
G SIGNLTNLRQVSLQNNNISGKI  
PPEICSLPKLQTLDLNNRFSGEI  
PGSVNQLSNLQYLRNLNNNSLSGPF  
5 PASLSQIPHLSFLDLSYNNLRGPV  
PKFPARTFNVAGNPLICKNS  
  
LPEICSGSISASPL  
SVSLRSSSGRRTN  
10  
ILAVALGVSLGFAVSVIL  
SLGFIWY  
  
RKKQRRLTMLRINKQEE  
15 GLLGLGNLRSFTFRELHVAT  
  
DGFSSKSILGAGGFGNVYRGKFGD  
GTVVAVKRLKDVNGTSGNSQFR  
TELEMISLAVHRNLLRLIGYCA  
20 SSSERLLVYPYMSNGSVASRLK  
AKPALDWNTRKKIAIGAA  
RGLFYLHEQCDPKIIHRDVKAA  
NILLDEYFEAVVGDFGLAKLLN  
HEDSHVTTAVRGTVGHIAPEYL  
25 STGQSSEKTDVFGFGILLLELI  
TGMRALEFGKSVSQKGAMLEW  
VRKLHKEMKVEELVDRELGTTY  
DRIEVGEMLQVALLCTQFLPAH  
RPKMSEVVQMLE  
30  
GDGLAERWAASHDHSFYHANM  
SYRTITSTDGNNQTKHLFG  
  
SSGFEDEDDNQALDSFAMELSGPR  
35

*Arabidopsis thaliana* RKS5 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctagagaattcttataactttttctacg**ATGGAGATT**CTTTGATGAAGTTTCTGTTTTTA  
GGAATCTGGGTTTATTATTACTCTGTTCTTGAAGTTTCTGCCATGGATAGTCTTTTA  
TCTCCCAAGGTGGCTGCCGTTAATGTCAGTGAAGAACAAGATGAAAGATGAGAAAGAGGTT  
TTGCTCTGGTTGGGATATTAACTCTGTTGATCCTTGACTTGAACATGGTTGGTTGTTCT  
TCTGAAGGTTTTGTGGTTTCTCTAGAGATGGCTAGTAAAGGATTATCAGGGATACTATCT  
15 ACTAGTATTGGGGAATTAACCTCATCTTCATACTTTGTTACTTCAGAATAATCAGTTAACT  
GGTCCGATTCTTCTGAGTTAGGCCAACTCTCTGAGCTTGAAACGCTTGATTATCGGGG  
AATCGGTTTAGTGGTGAAATCCCAGCTTCTTTAGGGTTCTTAACCTCACTTAACTACTTG  
CGGCTTAGCAGGAATCTTTATCTGGGCAAGTCCCTCACCTCGTCGCTGGCCTCTCAGGT  
CTTTCTTTCTTGGATCTATCTTTCAACAATCTAAGCGGACCAACTCCGAATATATCAGCA  
20 AAAGATTACAGGAAATGCATTTCTTTGTGGTCCAGCTTCCCAAGAGCTTTGCTCAGATGC  
TACACCTGTGAGAAATGCTGCAATCGATCTGCAGCGACGGGTTTGTCTGAAAAGGACAAT  
AGCAAACATCACAGCTTAGTGCTCTCTTTTGCATTTGGCATTGTTGTTGCCTTTATCATC  
TCCCTAATGTTTCTCTTCTTCTGGGTGCTTTGGCATCGATCACGTCTCTCAAGATCACAC  
GTGCAGCAAGACTACGAATTTGAAATCGGCCATCTGAAAAGGTTCAAGTTTTCGCGAAATA  
25 CAAACCGCAACAAGCAATTTTAGTCCAAAGAACATTTTGGGACAAGGAGGTTTGGGATG  
GTTTATAAAGGGTATCTCCCAAATGGAAGTGTGGTGGCAGTTAAAAGATTGAAAGATCCG  
ATTTATACAGGAGAAGTTCAGTTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTTTAC  
CGTAACCTTTTACGCCCTCTTTGGATTCTGTATGACCCCGAAGAGAGAATGCTTGTGTAT  
CCGTACATGCCAAATGGAAGCGTAGCTGATCGTCTGAGAGATTGGAATCGGAGGATAAGC  
30 ATTGCACTCGGCGCAGCTCGAGGACTTGTCTTACTTGACGAGCAATGCAATCCAAAGATT  
ATTCACAGAGACGTCAAAGCTGCAAATATTCTACTTGATGAGAGCTTTGAAGCAATAGTT  
GGCGATTTTGGTCTAGCAAAGCTTTTAGACCAGAGAGATTACATGTCACTACCGCAGTC  
CGAGGAACCATTTGGACACATCGCTCCCGAGTACCTTTCCACTGGACAGTCCTCAGAGAAA  
ACCGATGTTTTCGGATTTCGGAGTACTAATCCTTGAACCTATAACAGGTCTAAGATGATT  
35 GATCAAGGCAATGGTCAAGTTCGAAAAGGAATGATATTGAGCTGGGTAAGGACATTGAAA  
GCAGAGAAGAGATTTGCAGAGATGGTGGACAGAGATTTGAAGGGAGAGTTTGATGATTTG  
GTGTTGGAGGAAGTAGTGAATTTGGCTTTGCTTTGTACACAGCCACATCCGAATCTAAGA  
CCGAGGATGTCTCAAGTGTGAAGGTACTAGAAGGTTTAGTGGAACAGTGTGAAGGAGGG  
TATGAAGCTAGAGCTCCAAGTGTCTCTAGGAACTACAGTAATGGTCATGAAGAGCAGTCC  
40 TTTATTATTGAAGCCATTGAGCTCTCTGGACCACGATGAtagacttcatagtgtcttaac

tagtcttcttgattttgttgatgtcatggc

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS5 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains no
- 10 leucine zipper motif, in contrast to the other RKS proteins. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues.
- 15 The fifth domain contains many serine residues, and is likely to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine /
- 20 threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein /
- 25 protein interactions.

MEISLMKFLFLGIWVYYYS

VLDSVSAMDSLLSPKV

30

AALMSVKNMKDE

KEVLSGWDINSVD

PCTWNNMVGCSSEGFVVS

35

LEMASKGLSGILS

T SIGELTHLHTLLQNNQLTGPI

PSELGQLSELETDLDSGNRFSGEI

PASLGFLTHLNYLRSLRNLLSGQV

PHLVAGLSGLSFLDLSFNNLSGPT  
PNISAK DYRKCISLWSSFPR

ALLRCYTCEKCCNR  
5 SAATGLSEKDNSK

HHSLVLSFAFGIVV  
AFIISLMFLFFVWLWH

10 RSRLSRSHVQQDYEF  
EIGHLKRFSFREIQTAT

SNFSPKNILQGQFGMVYKGYLPN  
GTVVAVKRLKDPIYTGEVQFQ  
15 TEVEMIGLAVHRNLLRLEFGFCM  
TPEERMLVYPMPNGSVADRLR  
DWNRRISIALGAA  
RGLVYLHEQCNPKEIHRDVKAA  
NILLDESFEAIVGDFGLAKLLD  
20 QRDSHVTTAVRGTTIGHIAPEYL  
STGQSSEKTDVFGFVLELELI  
TGHKMIDQNGQVRKGMILSW  
VRTLKAEKRAEMVDRDLKGEF  
DDLVLVEEVVELALLCTQPHPNL  
25 RPRMSQVLKV

LEGLVEQCEGGYEARA

PASVSRNYSNGHEEQSFIEAIELSGPR  
30

*Arabidopsis thaliana* RKS6 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```
attgtttccttcttttgggattttctccttggtggaaccagctcaattaatgagatgag
10 ATGAGAATGTTTCAGCTTCGAGAAGATGGCTATGGCTTTTACTCTCTGTTTTTGCCTGT
TTATGCTCATTGTGTCTCCAGATGCTCAAGGGGATGCACTGTTTGCCTTGAGGATCTCC
TTACGTGCATTACCGAATCAGCTAAGTGACTGGAATCAGAACCAAGTTAATCCTTGCACT
TGGTCCCAAGTTATTTGTGATGACAAAACTTTGTCACCTCTTACATTGTCAGATATG
AACTTCTCGGGAACCTTGCTTCAAGAGTAGGAATCCTAGAAAATCTCAAGACTCTTACT
15 TTAAAGGGAAATGGAATTACGGGTGAAATACCAGAAGACTTTGGAAATCTGACTAGCTTG
ACTAGTTTGGATTGGAGGACAATCAGCTAACTGGTCGTATACCATCCACTATCGGTAAT
CTCAAGAACTTCAGTTCTTGACCTTGAGTAGGAACAACTTAATGGGACTATTCGGGAG
TCACTCACTGGTCTTCCAAACCTGTTAAACCTGCTGCTTGATTCCAATAGTCTCAGTGGT
CAGATTCTCAAAGTCTGTTTGAGATCCCAAAATATAATTCACGTCAAACAACTGAAT
20 TGTGGCGGTCGTC AACCTCACCCTTGTTGATCCGCGGTTGCCCATTCAGGTGATTCAAGC
AAGCCTAAACTGGCATTATTGCTGGAGTTGTTGCTGGAGTTACAGTTGTTCTCTTTGGA
ATCTTGTTGTTTCTGTTCTGCAAGGATAGGCATAAAGGATATAGACGTGATGTGTTTG
GATGTTGCAGGTGAAGTGGACAGGAGAATTGCATTTGGACAGTTGAAAAGGTTTGCATGG
AGAGAGCTCCAGTTAGCGACAGATAACTTCAGCGAAAAGAATGTACTTGGTCAAGGAGGC
25 TTTGGGAAAGTTTACAAAGGAGTGCTTCCGGATACACCCAAAGTTGCTGTGAAGAGATTG
ACGGATTTCGAAAGTCCTGGTGGAGATGCTGCTTCCAAAGGGAAGTAGAGATGATAAGT
GTAGCTGTTTCATAGGAATCTACTCCGTCTTATCGGGTTCTGCACCACACAAACAGAACGC
CTTTTGGTTTATCCCTTCATGCAGAATCTAAGTCTTGACATCGTCTGAGAGAGATCAAA
GCAGGCGACCCGGTTCTAGATTGGGAGACGAGGAAACGGATTGCCCTTAGGAGCAGCGCT
30 GGTTTTGAATATCTTCATGAACATTGCAATCCGAAGATCATACTCGTGATGTGAAAGCA
GCTAATGTGTTACTAGATGAAGATTTTGAAGCAGTGTTGGTGATTTTGGTTTAGCCAAG
CTAGTAGATGTTAGAAGGACTAATGTGACTACTCAAGTTCGAGGAACAATGGGTCACATT
GCACCAGAATATTTATCAACAGGGAAATCATCAGAGAGAACCGATGTTTTCGGGTATGGA
ATTATGCTTCTTGAGCTTGTTACAGGACAACCGCAATAGACTTTTTCACGTTTGGAGGAA
35 GAAGATGATGTCTTGTTACTTGACCACGTGAAGAACTGGAAAGAGAGAAGAGATTAGGA
GCAATCGTAGATAAGAATTTGGATGGAGAGTATATAAAGAAGAAGTAGAGATGATGATA
CAAGTGGCTTTGCTTTGTACACAAGGTTCAACAGAAGACCGACAGTGATGTCTGAAGTT
GTGAGGATGTTAGAAGGAGAAGGGCTTGCAGGAGAGATGGGAAGAGTGGCAAACCTGGAA
GTCACGAGACGTCATGAGTTTGAACGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCT
40 ATGCATAACCAAGATGCCATTGAATTATCTGGTGGAAGATGAacaaaaacatcaaacctt
```

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS6 protein.

Different domains are spaced and shown from the N-terminus  
5 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each  
10 separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain  
15 contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown  
20 function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single  
25 leucine rich repeat, probably involved in protein / protein interactions.

MRMFSL

QKMAMAFLLFFACLCSFVSPDAQG

30

DALFALRISLRALP

NQLSDWNQNQVN

PCTWSQVICDDKNEVTSL

35

TLSDMNFSGLSSRV

GILENLKTLTLKNGITGEI

PEDFGNLTSLTSLDLEDNQLTGRI

PSTIGNLKKLQFLTLNRNKLNGTI  
PESLTGLPNLLNLLLDNSLSGQI  
PQSLFEIPKYNFTSNNLNCGG

5 RQPHPCVSAVAHSGDSSKPKTG

IIAGVVAGVTVVL  
FGILLEFLFC

10 KDRHKGYYRDVFVDVAGE  
VDRRIAFGQLKRFARRELQLAT

DNFSEKNVLGQGGFGKVYKGVLPD  
TPKVAVKRLTDFESPGDAAFQ  
15 REDEMISVAVHRNLLRLIGFCT  
TQTERLLVYPFMQNLSLAHRLR  
EIKAGDPVLDWETRKRIALGAA  
RGFEYLHEHCNPKIIHRDVKAA  
NVLLDEDFEAVVGDFGLAKLVD

20 VRRTNVTTQVRGTMGHIAPEYL  
STGKSSERTDVFYGYIMLLELV  
TGQRAIDFSRLEEEDDVLLLDH  
VKKLEREKRLGAIVDKNLDGEY  
IKKEVEMMIQVALLCTQGSPE

25 RPVMSEVVRMLE

GEGLAERWEWQNVETRRHEFE

RLQRRFDWGEDSMHNQDAIELSGGR

30

*Arabidopsis thaliana* RKS7 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 acatccttgttttctgctcattcctctgtttcaaca**ATGGAGAGTACTATTGTTATGATGA**  
TGATGATAACAAGATCTTTCTTTTGCTTCTTGGGATTTTATGCCTTCTCTGCTCTTCTG  
TTCACGGATTGCTTTCTCCTAAAGGTGTTAACTTTGAAGTGAAGCTTTGATGGACATAA  
AAGCTTCATTACATGATCCTCATGGTGTCTTGATAACTGGGATAGAGATGCTGTTGATC  
CTTGTAGTTGGACAATGGTCACTTGTCTCTGAAAACCTTTGTCATTGGCTTAGGCACAC  
15 CAAGTCAGAATTTATCTGGTACACTATCTCCAAGCATTACCAACTTAACAAATCTTCGGA  
TTGTGCTGTTGCAGAACAAACATAAAAGGAAAAATTCCTGCTGAGATTGGTCGGCTTA  
CGAGGCTTGAGACTCTTGATCTTTCTGATAATTTCTTCCACGGTGAAATTCCTTTTTCAG  
TAGGCTATCTACAAAGCCTGCAATATCTGAGGCTTAACAACAATTCTCTCTCTGGAGTGT  
TTCCTCTGTCACTATCTAATATGACTCAACTTGCCTTTCTTGATTTATCATAACAACATC  
20 TTAGTGGTCCTGTTCCAAGATTTGCTGCAAAGACGTTTAGCATCGTTGGGAACCCGCTGA  
TATGTCCAACGGGTACCGAACAGACTGCAATGGAACAACATTGATACCTATGTCTATGA  
ACTTGAATCAAACCTGGAGTTCCTTTATACGCCGGTGGATCGAGGAATCACAAAATGGCAA  
TCGCTGTTGGATCCAGCGTTGGGACTGTATCATTAATCTTCATTGCTGTTGGTTTGTTC  
TCTGGTGGAGACAAAGACATAACCAAAACACATTCTTTGATGTTAAAGATGGGAATCATC  
25 ATGAGGAAGTTTCACTTGGAAACCTGAGGAGATTGGTTTCAGGGAGCTTCAGATTGCGA  
CCAATAACTTCAGCAGTAAGAACTTATGGGGAAAGGTGGCTATGGAAATGTATACAAAG  
GAATACTTGGAGATAGTACAGTGGTTCAGTGAAAAGGCTTAAAGATGGAGGAGCATTGG  
GAGGAGAGATTGAGTTTCAGACAGAAGTTGAAATGATCAGTTTAGCTGTTTCATCGAAATC  
TCTTAAGACTCTACGGTTTCTGCATCACACAAACTGAGAAGCTTCTAGTTTATCCTTATA  
30 TGTCTAATGGAAGCGTTGCATCTCGAATGAAAGCAAAACCTGTTCTTGACTGGAGCATAA  
GGAAGAGGATAGCCATAGGAGCTGCAAGAGGGCTTGTGTATCTCCATGAGCAATGTGATC  
CGAAGATTATCCACCGGATGTCAAAGCAGCGAATATACTTCTTGATGACTACTGTGAAG  
CTGTGGTTGGCGATTTTGGTTTAGCTAAACTCTTGATCATCAAGATTCTCATGTGACAA  
CCGCGGTTAGAGGCACGGTGGGTACATTGCTCCAGAGTATCTCTCAACTGGTCAATCCT  
35 CTGAGAAAACAGATGTTTTTGGCTTCGGGATTCCTTCTTCTTGAGCTTGTAACCGGACAAA  
GAGCTTTTGAGTTTGGTAAAGCGGCTAACAGAAAGGTGTGATGCTTGATTGGGTAAAAA  
AGATTCATCAAGAGAAGAACTTGAGCTACTTGTGGATAAAGAGTTGTTGAAGAAGAAGA  
GCTACGATGAGATTGAGTTAGACGAAATGGTAAGAGTAGCTTTGTTGTGCACACAGTACC  
TGCCAGGACATAGACCAAAAATGTCTGAAGTTGTTCAATGCTGGAAGGAGATGGACTTG  
40 CAGAGAAATGGGAAGCTTCTCAAAGATCAGACAGTGTTCAAAATGTAGCAACAGGATAA

ATGAATTGATGTCATCTTCAGACAGATACTCTGATCTTACCGATGACTCTAGTTTACTTG  
 TGCAAGCAATGGAGCTCTCTGGTCCTAGATGAaatctatacatgaatctgaagaagaaga  
 agaacatgcatctgtttcttgaatcaagagggattcttgtttttttgtataatagagagg  
 ttttttgagggaatgttgtgtctctgttaactgtataggcttgttgtgtaagaagttat  
 5 tactgcacttagggttaattcaaagttctttacataaaaaatgattagttgcgttgaata  
 gagggaaacactttgggagatttcatgtatgaaatttggaaaaaaaaaaaaaaaaaaaaa

10 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS7 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

15 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate  
 20 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-  
 25 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably  
 30 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

35

MESTIVMMMITRSFF  
 CFLGFLCCLCSSVHGLLSPKGVNFEV

QALMDIKASLHDP  
HGVLDNWDRDAVD

5 PCSWTMVTCSSENFVIG  
  
LGTSPQNLSGTL  
SPSITNLTLNRIVLLQNNNIKGKI  
PAEIGRLTRLETDLSDNFFHGEI  
PFSVGYLQSLQYLRLNNSLSGVF  
10 PLSLSNMTQLAFLDLSYNNLSGPV  
PRFAA KTF SIVGNPLICPT

GTEPDCNGTTLIPMSMNL  
NQTGVPLYAGGSRNHKMA  
15 IAVGSSVGTVSLIFIAVGLFLWW

RQRHNQNTFFDVKDNHHE  
EVSLGNLRRFGFRELQIAT  
20 NNFSSKNLLGKGGYGNVYKGILGD  
STVVAVKRLKDGGALGGEIQFQ  
TEVEMISLAVHRNLLRLYGFCI  
TQTEKLLVYPYMSNGSVA  
25 SRMKAKPVLDSIRKRIAIGAA  
RGLVYLHEQCDPKIIHRDVKAA  
NILLDDYCEAVVGDFGLAKLLD  
HQDSHVTTAVRGTVGHIAPEYL  
STGQSSEKTDVFGFGILLLELV  
30 TGQRAFEFGKAANQKGVMLDW  
VKKIHQEKKLELLVDKELLKKKSY  
DEIELDEMVRVALLCTQYLPGH  
RPKMSEVVRMLE

35 GDGLAEKWEASQRSDS  
VSKCSNRINELMSSS

DRYSDLTDDSSLLVQAMELSGPR

*Arabidopsis thaliana* RKS8 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 gtttttttttttttaccctcttgaggatctgggaggagaaatttgcttttttttggttaa  
ATGGGGAGAAAAAGTTTGAAGCTTTTGGTTTGTCTGCTTAATCTCACTGCTTCTTCTG  
TTTAATTCGTTATGGCTTGCCTCTTCTAACATGGAAGGTGATGCACTGCACAGTTTGAGA  
GCTAATCTAGTTGATCCAAATAATGTCTTGCAAAGCTGGGATCCTACGCTTGTTAATCCG  
TGTACTTGGTTTTCAGTAACGTGTAACAACGAGAACAGTGTTATAAGAGTCGATCTTGGG  
15 AATGCAGACTTGTCTGGTCAGTTGGTTCCTCAGCTAGGTCAGCTCAAGAACTTGCAGTAC  
TTGGAGCTTTATAGTAATAACATAACCGGGCCGGTCCAAGCGATCTTGGGAATCTGACA  
AACTTAGTGAGCTTGGATCTTTACTTGAACAGCTTCACTGGTCCAATTCCAGATTCTCTA  
GGAAAGCTATTCAAGCTTCGC'TTCTTCGGCTCAACAATAACAGTCTCACCGGACCAATT  
CCCATGTCATTGACTAATATCATGACCCCTTCAAGTTTGGATCTGTGCAACAACCGATTA  
20 TCCGGATCTGTTCCGTGATAATGGTTCCTTCTCGCTCTTCACTCCCATCAGTTTGTCTAAC  
AACTTGGATCTATGCGGCCAGTTACTAGCCGTCCTTGTCTGGATCTCCCCCGTTTCT  
CCTCCACCACCTTTTATACCACCTCCCATAGTTCTTACACCAGGTGGGTATAGTGCTACT  
GGAGCCATTGCGGGAGGAGTTGCTGCTGGTGCTGCTTACTATTGCTGCCCCGTGCTTGA  
GCTTTTGCTTGGTGGCGTAGAAGAAACCTCAAGAATTCTTCTTTGATGTTCTGCGCGAA  
25 GAGGACCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCTACGGGAACCTCAAGTA  
GCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCCGAGGTGGGTTGCGAAAAGTCTAC  
AAAGCCCGTCTTGTGATGGAACACTTGTGTCAGTCAAACGGCTTAAAGAAGAGCGAACC  
CCAGGTGGCGAGCTCCAGTTTCAGACAGAAGTGGAGATGATAAGCATGGCCGTTACAGA  
AATCTCCTCAGGCTACGCGGTTTCTGTATGACCCCTACCGAGAGATTGCTTGTATTATCCT  
30 TACATGGCTAATGGAAGTGTGCTTCTGTTTGTGAGAGAACGTCCACCATCACAGTTGCCT  
CTAGCCTGGTCAATAAGACAGCAAATCGCGCTAGGATCAGCGAGGGGTTTGTCTTATCTT  
CATGATCATTGCGACCCCAAATATTACCGTGATGTGAAAGCTGCTAATATTCTGTTG  
GACGAGGAATTTGAGGCGGTGGTAGGTGATTTGCGGTAGCTAGACTTATGGACTATAAA  
GATACTCATGTCAACGGCTGTGCGTGGGACTATTGGACACATTGCTCCTGAGTATCTC  
35 TCAACTGGAAAATCTTCAGAGAAAACGATGTTTTTGGCTACGGGATCATGCTTTTGGA  
CTGATTACAGGTGAGAGAGCTTTTGATCTTGCAAGACTGGCGAATGACGATGACGTTATG  
CTCCTAGATTGGGTGAAAGGGCTTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCCT  
GACCTGCAAAGCAATTACACAGAAGCAGAAGTAGAACAGCTCATACAAGTGGCTCTTCTC  
TGCACACAGAGCTCACCTATGGAACGACCTAAGATGTCTGAGGTTGTTGCAATGCTTGAA  
40 GGTGACGGTTTAGCGGAGAAATGGGACGAGTGGCAGAAAGTGGAAGTTCTCAGGCAAGAA

GTGGAGCTCTCTTCTACCCACCTCTGACTGGATCCTTGATTGACTGATAATCTTCAT  
GCTATGGAGTTGTCTGGTCCAAGATAAacgacattgtaatttgcctaacagaaaagagaa  
agaacagagaaaatattaagagaatcacttctctgtattctt

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS8 protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino  
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline  
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also  
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30 MGRKKFEAFGFVCLISLLLLFNSL  
WLASSNMEG

DALHSLRANLVDP  
NNVLQSWDPTLVN

35

PCTWFHVTCNNNSVIRV

DLGNADLSGQLV

P QLGQLKNLQYLELYSNNITGPV

40 PSDLGNLTNLVSLDLYLNSFTGPI

PDSLGLKLFKLRFLRLNNSLTGPI  
PMSLTNIMTLQVLDLSNNRLSGSV  
PDNGSFSLFTPISFANNLDLCGPV

5   TSRPCPGSPFFSPPPP  
     FIPPPIVPTPGGYSATG

AIAGGVAAGAAL  
LFAAPALAFWW

10   RRRKPOEFFFDVPAEEDPE  
     VHLGQLKRFSLRELQVAT

DSFSNKNILGRGGFGKVYKGRAD  
15   GTLVAVKRLKEERTPGGELQFQ  
     TEVEMISMAVHRNLLRLRGFCM  
     TPTERLLVYPYMANGSVASCLR  
     ERPPSQLPLAWSIRQQIALGSA  
     RGLSYLHDHCDPKIIHRDVKAA

20   NILLDEEFEAVVGDFGLARLMD  
     YKDTHVTTAVRGITIGHIAPEYL  
     STGKSSEKTDVFGYGIMLLELI  
     TGQRAFDLARIANDDDVMLLDW  
     VKGLLKEKKLEMLVDPDLQSNY

25   TEAEVEQLIQVALLCTQSSPME  
     RPKMSEVVRMLE

GDGLAEKWDEWQKVEVLRQEVLS

30   SHPTSDWILDSTDNLHAMELSGPR

*Arabidopsis thaliana* rks10 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atcagggggttttaacaatgatggatctctctgatgagggatagttctagggtttgttt  
taatctcttgaggataaaa**ATGGAACGAAGATTAATGATCCCTTGCTTCTTTTGGTTGATT**  
CTCGTTTTGGATTGGTTCTCAGAGTCTCGGGCAACGCCGAAGGTGATGCTCTAAGTGCA  
CTGAAAAACAGTTTAGCCGACCCTAATAAGGTGCTTCAAAGTTGGGATGCTACTCTTGTT  
ACTCCATGTACATGGTTTTCATGTTACTTGCAATAGCGACAATAGTGTTACACGTGTGAC  
15 CTTGGGAATGCAAATCTATCTGGACAGCTCGTAATGCAACTTGGTCAGCTTCCAACTTG  
CAGTACTTGGAGCTTTATAGCAATAACATTACTGGGACAATCCCAGAACAGCTTGGAAAT  
CTGACGGAATTGGTGAGCTTGGATCTTACTTGAACAATTTAAGCGGGCCTATTCCATCA  
ACTCTCGGCCGACTTAAGAACTCCGTTTCTTGCCTCTTAATAACAATAGCTTATCTGGA  
GAAATTCGAAGTCTTTGACTGCTGTCTGACGCTACAAGTTCTGGATCTCTCAAACAAT  
20 CCTCTCACCGGAGATATTCCTGTTAATGGTTCCTTTTCACTTTTCACTCCAATCAGTTTT  
GCCAACACCAAGTTGACTCCCTTCTGTCATCTCCACCGCCTCCTATCTCTCCTACACCG  
CCATCACCTGCAGGGAGTAATAGAATTACTGGAGCGATTGCGGGAGGAGTTGCTGCAGGT  
GCTGCACTTCTATTTGCTGTTCCGGCCATTGCACTAGCTTGGTGGCGAAGGAAAAAGCCG  
CAGGACCACTTCTTTGATGTACCAGCTGAAGAGGACCCAGAAGTTCATTTAGGACAACCTG  
25 AAGAGGTTTTTCATTGCGTGAACACTACAAGTTGCTTCGGATAATTTTAGCAACAAGAACATA  
TTGGGTAGAGGTGGTTTTTGGTAAAGTTTATAAAGGACGGTTAGCTGATGGTACTTTAGTG  
GCCGTTAAAAGGCTAAAAGAGGAGCGCACCCAAAGGTGGCGAACTGCAGTTCAGACAGAG  
GTTGAGATGATTAGTATGGCGGTTACAGAACTTGCTTCGGCTTCGTGGATTTTGCAATG  
ACTCCAACCGAAAGATTGCTTGTATCCCTACATGGCTAATGGAAGTGTGCCTCCTGT  
30 TTAAGAGAACGTCCCGAGTCCCAGCCACCACTTGATTGGCCAAAGAGACAGCGTATTGCG  
TTGGGATCTGCAAGAGGGCTTGCCTATTTACATGATCATTGCGACCCAAAGATTATTCAT  
CGAGATGTGAAAGCTGCAAAATATTTTGTGGATGAAGAGTTTGAAGCCGTGGTTGGGGAT  
TTTGGACTTGCAAACTCATGGACTACAAAGACACACATGTGACAACCGCAGTGCCTGGG  
ACAATTGGTCATATAGCCCTGAGTACCTTTCCACTGGAAAATCATCAGAGAAAACCGAT  
35 GTCTTTGGGTATGGAGTCATGCTTCTTGAGCTTATCACTGGACAAAGGGCTTTTGATCTT  
GCTCGCCTCGCGAATGATGATGATGTGATGTTACTAGACTGGGTGAAAGGGTTGTTAAAA  
GAGAAGAAATTGGAAGCACTAGTAGATGTTGATCTTCAGGGTAATTACAAAGACGAAGAA  
GTGGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGAGTTCACCAATGGAAAGACCC  
AAAATGTCTGAAGTTGTAAGAATGCTTGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAG  
40 TGGCAAAAGGAGGAAATGTTGAGACAAGATTTCAACTACCCAACCCACCATCCAGCCGTG

TCTGGCTGGATCATTGGCGATTCCACTTCCCAGATCGAAAACGAATACCCCTCGGGTCCA  
AGATAAagattcgaaacacgaatgttttttctgtattttgttttctctgtatttattgag  
ggtttttagcttc

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS10 protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as  
described in Schmidt et al. (1997).  
At the predicted extracellular domain the first domain represents a  
signal sequence. The second domain contains a leucine zipper motif,  
containing 4 leucine residues, each separated by seven other amino  
15 acids. The third domain contains conserved cysteine residues,  
involved in disulphate bridge formation. The fourth domain contains a  
leucine rich repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain contains many  
serine and proline residues, and is likely to contain hydroxy-proline  
20 residues, and to be a site for O-glycosylation. The sixth domain  
contains a single transmembrane domain after which the predicted  
intracellular domains are positioned. The seventh domain has an  
unknown function. The eighth domain represents a serine / threonine  
protein kinase domain (Schmidt et al. 1997) and is probably also  
25 containing sequences for protein / protein interactions. The ninth  
domain has an unknown function. The last and tenth domain at the C-  
terminal end represents part of a single leucine rich repeat,  
probably involved in protein / protein interactions.

30 MERRLMIPCFFWLILVL  
DLVLRVSGNAEG

DALSALKNSLADP  
NKVLQSWDATLVT

35 PCTWFHVTCNSDNSVTRV

DLGNANLSGQLV  
M QLGQLPNLQYLELYSNNITGTI  
40 PEQLGNLTELVS LDLYLNNLSGPI

PSTLGRLKKLRFLRLNNNSLSGEI  
PRSLTAVLTLQVLDLSNNPLTGDI  
PVNGSFSLTPISFANTK LT PL

5 PASPPPPISPTPPSPAGSNRITG

AIAGGVAAGAAL  
LFAVPAIALAWW

10 RRKKPQDHFFDVPAEEDPE  
VHLGQLKRFSLRELQVAS

DNFSNKNILGRGGFGKVYKGRLAD  
GTLVAVKRLKEERTQGGELOFQ  
15 TEVEMISMAVHRNLLRLRGFCM  
TPTERLLVYPYMANGSVASCLR  
ERPESQPPLDWPKRQRIALGSA  
RGLAYLHDHCDPKIIHRDVKAA  
NILLDEEFEAVVGDFGLAKLMD  
20 YKOTHVTTAVRGTTIGHIAPEYL  
STGKSSEKTDVFGYGVMLLELI  
TGQRAFDLARLANDDDVMLLDW  
VKGLLKEKKLEALVDVDLQGNV  
KDEEVEQLIQVALLCTQSSPME  
25 RPKMSEVVRMLE

GDGLAERWEEWQKEEMFRQDFNYPTH

PAVSGWIIGDSTSQIENEYPSGPR

30

*Arabidopsis thaliana* RKS 11 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttgttaacctctcgttaactaaaatcttcc**ATGG**TAGTAGTAACAAAGAAGACCATGAAGA  
TTCAAATTCATCTCCTTTACTCGTTCTTGTTCCTCTGTTTCTCTACTCTCACTCTATCTT  
CTGAGCCCAGAAACCTGAAGTTGAGGCGTTGATAAGTATAAGGAACAATTTGCATGATC  
CTCATGGAGCTTTGAACAATTGGGACGAGTTTTCAGTTGATCCTTGTAGCTGGGCTATGA  
TCACTTGCTCTCCCGACAACCTCGTCATTGGACTAGGAGCGCCGAGCCAGTCTCTCTCGG  
15 GAGGTTTATCTGAGTCTATCGGAAATCTCACAATCTCCGACAAGTGTCATTGCAAAATA  
ACAACATCTCCGGCAAAATCCACCGGAGCTCGGTTTCTACCCAAATTACAAACCTTGG  
ATCTTTCCAACAACCGATTCTCCGGTGACATCCCTGTTTCCATCGACCAGCTAAGCAGCC  
TTCAATATCTGAGACTCAACAACAACCTCTTGTCTGGGCCCTTCCCTGCTTCTTTGTCCC  
AAATTCCTCACCTCTCCTTCTTGACTTGTCTTACAACAATCTCAGTGGCCCTGTTCCCTA  
20 AATTCACGCAAGGACTTTAAACGTTGCTGGTAATCCTTTGATTGTAGAAGCAACCCAC  
CTGAGATTTGTTCTGGATCAATCAATGCAAGTCCACTTTCTGTTTCTTTGAGCTCTTCAT  
CAGGACGCAGGTCTAATAGATTGGCAATAGCTCTTAGTGTAAGCCTTGGCTCTGTTGTTA  
TACTAGTCCTTGCTCTCGGGTCTTTTGTGTTGTAACGAAAGAAACAAAGAAGGCTACTGA  
TCCTTAACTTAAACGCAGATAAACAAGAGGAAGGGCTCAAGGACTTGGGAATCTAAGAA  
25 GCTTCACATTCAAGAACTCCATGTTTATACAGATGGTTTCAGTTCCAAGAACATTCTCG  
GCGCTGGTGGATTCCGTAATGTGTACAGAGGCAAGCTTGGAGATGGGACAATGGTGGCAG  
TGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTCACAGTTTCGTATGGAGCTAG  
AGATGATTAGCTTAGCTGTTCATAAGAATCTGCTTCGGTTAATTGGTTATTGCGCAACTT  
CTGGTGAAAGGCTTCTGTTTACCCTTACATGCCTAATGGAAGCGTCGCCTCTAAGCTTA  
30 AATCTAAACCGGCATTGGACTGGAACATGAGGAAGAGGATAGCAATTGGTGCAGCGAGAG  
GTTTGTGTATCTACATGAGCAATGTGATCCCAAGATCATTCATAGAGATGTAAAGGCAG  
CTAATATTCTCTTAGACGAGTGCTTTGAAGCTGTTGTTGGTGACTTTGGACTCGCAAAGC  
TCCTTAACCATGCGGATTCTCATGTCACAACTGCGGTCCGTGGTACGGTTGGCCACATTG  
CACCTGAATATCTCTCCACTGGTCAGTCTTCTGAGAAAACCGATGTGTTTGGGTTCGGTA  
35 TACTATTGCTCGAGCTCATAACCGGACTGAGAGCTCTTGAGTTTGGTAAAACGTTAGCC  
AGAAAGGAGCTATGCTTGAATGGGTGAGGAAATTACATGAAGAGATGAAAGTAGAGGAAC  
TATTGGATCGAGAACTCGGAACTAACTACGATAAGATTGAAGTTGGAGAGATGTTGCAAG  
TGGCTTTGCTATGCACACAATATCTGCCAGCTCATCGTCTAAAATGTCTGAAGTTGTTT  
TGATGCTTGAAGGCGATGGATTAGCCGAGAGATGGGCTGCTTCGCATAACCATTACATT  
40 TCTACCATGCCAATATCTCTTCAAGACAATCTCTTCTGTCTACTACTTCTGTCTCAA

GGCTTGACGCACATTGCAATGATCCAACCTTATCAAATGTTTGGATCTTCGGCTTTCGATG  
 ATGACGATGATCATCAGCCTTTAGATTCCCTTGCCATGGAAGTATCCGGTCCAAGATAAc  
 acaatgaaagaaagatatcattttttacgatggatcaaacaatccaatgaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
 RKS11 protein.

10 Different domains are spaced and shown from the N-terminus  
 towards the C-terminus. Overall domain structure is similar as  
 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain  
 represents a signal sequence. The second domain contains a  
 15 leucine zipper motif, containing 3 leucine residues, each  
 separated by seven other amino acids. The third domain  
 contains conserved cysteine residues, involved in disulphate  
 bridge formation. The fourth domain contains a leucine rich  
 repeat domain, consisting of 5 complete repeats of each  
 20 approximately 24 amino acid residues. The fifth domain  
 contains many serine and proline residues, and is likely to  
 contain hydroxy-proline residues, and to be a site for O-  
 glycosylation. The sixth domain contains a single  
 transmembrane domain after which the predicted intracellular  
 25 domains are positioned. The seventh domain has an unknown  
 function. The eight domain represents a serine / threonine  
 protein kinase domain (Schmidt et al. 1997) and is probably  
 also containing sequences for protein / protein interactions.  
 The ninth domain has an unknown function. The last and tenth  
 30 domain at the C-terminal end represents part of a single  
 leucine rich repeat, probably involved in protein / protein  
 interactions.

MVVVTKKTMKIQIHLLYSFLFL  
 35 CFSTLTLSSEPRNPEV

EALISIRNNLHDP  
 HGALNNWDEFSVD

PCSWAMITCSPDNLVIGL

GAPSQSLSGGLS

5   ESIGNLTNLRQVSLQNNNISGKI  
PPELGFLPKLQTLDLSENRFSGDI  
PVSIDQLSSLQYLRLNNSLSGPF  
PASLSQIPHLSFLDLSYNNLSGPV  
PKFPARTFNVAGNPLICRSN

10   PPEICSGSINASPL  
SVSLSSSSGRRSNR

LAIALSVSLGSVVIL  
15   VLALGSFCWY

RKKQRRLLILNLNGADKQEE  
GLQGLGNLRSFTFRELHVYT

20   DGFSSKNILGAGGFENVYRGKLG  
GTMVAVKRLKDINGTSGDSQFR  
MELEMISLAVHKNNLLRLIGYCA  
TSGERLLVYPMPNGSVASKLK  
SKPALDWNMRKRIAIGAA

25   RGLLYLHEQCDPKIIHRDVKAA  
NILLDECFEAVVGDFGLAKLLN  
HADSHVTTAVRGTVGHIAPEYL  
STGQSSEKTDVFGFGILLLELI  
TGLRALEFGKTVSQKGAMLEW

30   VRKLHEEMKVEELLDRELGTNY  
DKIEVGEMLQVALLCTQYLPAA  
RPKMSEVVLMLE

GDGLAERWAASHNHSHFYHANI  
35   SFKTISSLSTTSVSRDLAHCNDPTYQMFG

SSAFDDDDHQPLDSFAMELSGPR

*Arabidopsis thaliana* RKS12 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tttaaaaaccttgctagttctcaattctcatgactttgcttttagtcttagaagtggaaa  
ATGGAACATGGATCATCCCGTGGCTTTATTGGCTGATTCTATTTCTCGATTTGTTTCC  
AGAGTCACCGGAAAAACACAAGTTGATGCTCTCATTGCTCTAAGAAGCAGTTTATCATCA  
GGTGACCATACAAACAATATACTCCAAAGCTGGAATGCCACTCACGTTACTCCATGTTCA  
TGGTTTCATGTTACTTGCAATACTGAAAACAGTGTTACTCGTCTGACCTGGGGAGTGCT  
15 AATCTATCTGGAGAACTGGTGCCACAGCTTGCTCAGCTTCCAAATTTGCAGTACTTGGAA  
CTTTTAAACAATAATATTACTGGGGAGATACCTGAGGAGCTTGGCGACTTGATGGAATA  
GTAAGCTTGGACCTTTTTGCAAACAACATAAGCGGTCCCATCCCTTCTCTTGGCAAA  
CTAGGAAAACCTCCGCTTCTTGCGTCTTTATAACAACAGCTTATCTGGAGAAATCCAAGG  
TCTTTGACTGCTCTGCCGCTGGATGTTCTTGATATCTCAAACAATCGGCTCAGTGGAGAT  
20 ATTCTGTTAATGGTTCCTTTTCGCAGTTCACCTTCTATGAGTTTGGCAATAATAAATTA  
AGGCCGCGACCTGCATCTCCTTCACCATCACCTTCAGGAACGCTGCAGCAATAGTAGTG  
GGAGTTGCTGCGGGTGCACTTCTATTTGCGCTTGCTTGGTGGCTGAGAAGAAAACCTG  
CAGGGTCACCTTTCTTGATGTACCTGCTGAAGAAGACCCAGAGGTTTATTTAGGACAATTT  
AAAAGGTTCTCCTTGCGTGAAGTGTAGTTGCTACAGAGAAATTTAGCAAAAGAAATGTA  
25 TTGGGCAAAGGACGTTTTTGGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGTG  
GCTGTGAAACGGCTAAATGAAGAACGTACCAAGGGTGGGGAACGTCAGTTTCAAACCGAA  
GTTGAGATGATCAGTATGGCCGTTTCATAGGAACCTGCTTCGGCTTCGTGGCTTTTGCATG  
ACTCCAACCTGAAAGATTACTTGTTTATCCCTACATGGCTAATGGAAGTGTGCTTCTTGT  
TTAAGAGAGCGTCTGAAGGCAATCCAGCCCTTGACTGGCCAAAAAGAAAGCATATTGCT  
30 CTGGGATCAGCAAGGGGGCTCGCATATTTACACGATCATTGCGACCAAAAGATCATTCAC  
CTGGATGTGAAAGCTGCAAATATACTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGAT  
TTTGGGCTAGCAAAATTAATGAATTATAACGACTCCCATGTGACAACTGCTGTACGGGGT  
ACGATTGGCCATATAGCGCCCGAGTACCTCTCGACAGGAAAATCTTCTGAGAAGACTGAT  
GTTTTTGGGTACGGGGTCATGCTTCTCGAGCTCATCACTGGACAAAAGGCTTTTCGATCTT  
35 GCTCGGCTTGCAAATGATGATGATATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAA  
GAGAAGAAGTTGGAAGCCTTGTGGATGCAGAACTCGAAGGAAAGTACGTGGAACAGAA  
GTGGAGCAGCTGATACAAATGGCTCTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCA  
AAGATGTCAGAAGTAGTGAGAATGCTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAA  
TGGCAAAAGGAGGAGATGCCAATACATGATTTTAACTATCAAGCCTATCCTCATGCTGGC  
40 ACTGACTGGCTCATCCCTATTCCAATTCCTTATCGAAAACGATTACCCCTCGGGGCCA

AGATAAaccttttagaaagggtcatttcttgtgggttcttcaacaagtatatataggtta  
gtgaagttgtaagaagcaaaacccacattcacctttgaatatcactactctataa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS12 protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as  
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain  
represents a signal sequence. The second domain contains a  
leucine zipper motif, containing 2 leucine residues, each  
15 separated by seven other amino acids. The third domain  
contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich  
repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain  
20 contains many serine and proline residues, and is likely to  
contain hydroxy-proline residues, and to be a site for O-  
glycosylation. The sixth domain contains a single  
transmembrane domain after which the predicted intracellular  
domains are positioned. The seventh domain has an unknown  
25 function. The eighth domain represents a serine / threonine  
protein kinase domain (Schmidt et al. 1997) and is probably  
also containing sequences for protein / protein interactions.  
The ninth domain has an unknown function. The last and tenth  
domain at the C-terminal end represents part of a single  
30 leucine rich repeat, probably involved in protein / protein  
interactions.

MEHGSSRGFI

WLILFLDFVSRVTGKTQV

35

DALIALRSSLSSGDHTNNILQ

SWNATHVT

PCSWFHVTCNTENSVTRL

DLGSANLSGELV

P QLAQLPNLQYLELFNNITGEI  
5 PEELGDLMELVSLDLFANNISGPI  
PSSLGKLGKLRFLRLYNNSLSGEI  
PRSLTALP LDVLDISNNRLSGDI  
PVNGSFSQFTSMRFA NNKLRRPR

10 PASPSPSPSGGTS

AAIVVGVAAGAALLFALAWWL

RRKLQGHFLDVPAAEEDPE  
15 VYLGQFKRFSRLRELLVAT

EKFSKRNVLGKGRFGILYKGR LAD  
DTLVAVKRLNEERTKGGELQFQ  
TEVEMISMAVHRNLLRLRGFCM  
20 TPTERLLVYPYMANGSVASCLR  
ERPEGNPALDWPKRKHIALGSA  
RGLAYLHDHCDQKIIHL DVKAA  
NILLDEEFEAVVGDFGLAKLMN  
YNDSHVTTAVRG TIGHIAPEYL  
25 STGKSSEKTDVFGYGVMLLELI  
TGQKAFDLARLANDDDIMLLDW  
VKEVLKEKKLES LVD AELEGKY  
VETEVEQLIQMALLCTQSSAME  
RPKMSEVVRMLE

30 GDGLAERWE EWQKEEMPIHDFNYQAY

PHAGTDWLIPYSNSLIENDYPSGPR

35

*Arabidopsis thaliana* RKS13 cDNA

The start codons encoding predicted the methionine residue of the gene product has been indicated by bold capitals. The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

taataaacctctaataataatggctttgcttttactctgatgacaagttcaaaa**ATGGAA**  
10 CAAAGATCACTCCTTTGCTTCCTTTATCTGCTCCTACTATTCAATTTCACTCTCAGAGTC  
GCTGGAAACGCTGAAGGTGATGCTTTGACTCAGCTGAAAAACAGTTTGTATCAGGTGAC  
CCTGCAAACAATGTACTCCAAAGCTGGGATGCTACTCTTGTACTCCATGTACTTGGTTT  
CATGTTACTTGCAATCCTGAGAATAAAGTTACTCGTGTGACCTTGGGAATGCAAACTA  
TCTGGAAAGTTGGTTCCAGAACTTGGTCAGCTTTTAACTTGCAGTACTTGGAGCTTTAT  
15 AGCAATAACATTACAGGGGAGATACCTGAGGAGCTTGGCGACTTGGTGAAGTAGTAAGC  
TTGGATCTTTACGCAAACAGCATAAGCGGTCCCATCCCTTCGTCTCTTGGCAAACCTAGGA  
AAACTCCGTTCTTGGCTCTTAACAACAATAGCTTATCAGGGGAAATCCAATGACTTTG  
ACTTCTGTGCAGCTGCAAGTTCTGGATATCTCAAACAATCGGCTCAGTGGAGATATTCCT  
GTTAATGGTTCTTTTCGCTCTTCACTCCTATCAGTTTGGCAATAATAGCTTAACGGAT  
20 CTTCCCGAACCTCCGCTACTTCTACCTCTCCTACGCCACCACCACCTTCAGGGGGGCAA  
ATGACTGCAGCAATAGCAGGGGAGTTGCTGCAGGTGCAGCACTTCTATTGCTGTTCCA  
GCCATTGCGTTTGCTTGGTGGCTCAGAAGAAAACACAGGACCACCTTTTTTGATGTACCT  
GCTGAAGAAGACCCAGAGGTTCAATTTAGGACAACCTCAAAGGTTTACCTTGCGTGAAGTG  
TTAGTTGCTACTGATAACTTTAGCAATAAAAATGTATTGGGTAGAGGTGGTTTGGTAAA  
25 GTGTATAAAGGACGTTTAGCCGATGGCAATCTAGTGGCTGTCAAAGGCTAAAAGAAGAA  
CGTACCAAGGGTGGGGAAGTGCAGTTTCAAACCGAAGTTGAGATGATCAGTATGGCCGTT  
CATAGGAAGTTGCTTCGGCTTCGTGGCTTTTGCATGACTCCAAGTAAAGATTACTTGTT  
TATCCCTACATGGCTAATGGAAGTGTGCTTCTGTTTAAAGAGCGTCCTGAAGGCAAT  
CCAGCACTTGATTGGCCAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTTGCG  
30 TATTTACATGATCATTGCGACCAAAAAATCATTACCGGGATGTTAAAGCTGCTAATATA  
TTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGATTTTGGGCTCGCAAAATTAATGAAT  
TATAATGACTCCCATGTGACAACTGCTGTACGCGGTACAATTGGCCATATAGCGCCCGAG  
TACCTCTCGACAGGAAAATCTTCTGAGAAGACTGATGTTTTTGGGTACGGGTCATGCTT  
CTCGAGCTCATCACTGGACAAAAGGCTTTCGATCTTGCTCGGCTTGCAAATGATGATGAT  
35 ATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAAGAGAAGAAGTTGGAAAGCCTTGTG  
GATGCAGAACTCGAAGGAAAGTACGTGGAACAGAAGTGGAGCAGCTGATACAAATGGCT  
CTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCAAGATGTCAGAAGTAGTGAGAATG  
CTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAATGGCAAAAGGAGAGATGCCAATA  
CATGATTTTAACTATCAAGCCTATCCTCATGCTGGCACTGACTGGCTCATCCCTATTCC  
40 AATTCCTTATCGAAAACGATTACCCCTCGGGTCCAAGATAAccttttagaaaggtctt

ttcttggtgggttcttcaacaagtatatatatagattggtgaagttttaagatgcaaaaaa  
aa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS13 protein.

Different domains are spaced and shown from the N-terminus  
towards the C-terminus. Overall domain structure is similar as  
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain  
represents a signal sequence. The second domain contains  
leucine zipper motifs, containing 2 times 2 leucine residues,  
each separated by seven other amino acids. The third domain  
15 contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich  
repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain  
contains many serine and proline residues, and is likely to  
20 contain hydroxy-proline residues, and to be a site for O-  
glycosylation. The sixth domain contains a single  
transmembrane domain after which the predicted intracellular  
domains are positioned. The seventh domain has an unknown  
function. The eighth domain represents a serine / threonine  
25 protein kinase domain (Schmidt et al. 1997) and is probably  
also containing sequences for protein / protein interactions.  
The ninth domain has an unknown function. The last and tenth  
domain at the C-terminal end represents part of a single  
leucine rich repeat, probably involved in protein / protein  
30 interactions.

MEQRSLLCFLYLL  
LLFNFTLRVAGNAEG

35 DALTQLKNSLSSGDP  
ANNVLQSWDATLVT

PCTWFHVTCNPENKVTRV

DLGNAKLSGKLV  
P ELGQLLNLYLELYSNNITGEI  
PEELGDLVELVSLDLYANSISGPI  
5 PSSLGKLGKLRFLRLNNSLSGEI  
PMTLTSVQLQV LDISNNRLSGDI  
PVNGSFSLFTPISFANNSLTDLPE  
  
PPPTSTSPTPPPPSG  
10 GQMTAAIAGGVAAGAAL  
LFAVPAIAFAWWL  
  
RRKPQDHFFDVPGAEDPE  
15 VHLGQLKRFTLRELLVAT  
  
DNFSNKNVLGRGGFGKVYKGRAD  
GNLVAVKRLKEERTKGGELQFQ  
TEVEMISMAVHRNLLRLRGFCM  
20 TPTERLLVYPYMANGSVASCLR  
ERPEGNPALDWPKRKHIALGSA  
RGLAYLHDHCDQKIIHRDVKAA  
NILLDEEFEAVVGDFGLAKLMN  
YNDSHVTTAVRG TIGHIAPEYL  
25 STGKSSEKTDVFGYGVMLLELI  
TGQKAFDLARLANDDDIMLLDW  
VKEVLKEKKLESIVDAELEGKY  
VETEVEQLIQMALLCTQSSAME  
RPKMSEVVRMLE  
30 GDGLAERWEEWQKEEMPIHDFNYQA  
  
YPHAGTDWLIPYSNSLIENDYPSGPR

35

*Arabidopsis thaliana* RKS14 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctgcaccttagagattaataactctcaagaaaaacaagttttgattcggacaaag**ATG**TTG  
CAAGGAAGAAGAGAAGCAAAAAGAGTTATGCTTTGTTCTCTCAACTTTCTTCTTCTC  
TTTATCTGTTTTCTTCTTCTTCTTCTGCGAAGTCTACAGACAAAGTTGTTGCCTTAATA  
GGAATCAAAGCTCACTGACTGATCCTCATGGAGTTCTAATGAATTGGGATGACACAGCA  
GTTGATCCATGTAGCTGGAACATGATCACTTGTCTGATGGTTTTGTCATAAGGCTAGAA  
15 GCTCCAAGCCAAAACCTTATCAGGAACCTTTTCATCAAGTATTGGAAATTTAACAAATCTT  
CAAACGTATACAGGTTATTGCGAACAATTACATAACAGGAAACATCCCTCATGAGATT  
GGGAAATTGATGAAACTCAAACACTTGATCTCTCTACCAATAACTTCACTGGTCAAATC  
CCATTCACTCTTTCTTACTCCAAAATCTTCACAGGAGGGTTAATAATAACAGCCTGACA  
GGAACAATTCCTAGCTCATTGGCAAACATGACCCAACTCACTTTTTGGATTTGTCGTAT  
20 AATAACTTGAGTGGACCAGTTCCAAGATCACTTGCCAAAACATTCAATGTTATGGGCAAT  
TCTCAGATTTGTCCAACAGGAACGAGAAAGACTGTAATGGGACTCAGCCTAAGCCAATG  
TCAATCACCTTGAACAGTTCTCAAAGAACTAAAAACCGGAAAATCGCGGTAGTCTTCGGT  
GTAAGCTTGACATGTGTTTGCTTGTGATCATTGGCTTTGGTTTTCTTCTTTGGTGGAGA  
AGAAGACATAACAAACAAGTATTATTCTTTGACATTAATGAGCAAAACAAGGAAGAAATG  
25 TGTCTAGGGAATCTAAGGAGGTTAATTTCAAAGAACTTCAATCCGCAACTAGTAACCTC  
AGCAGCAAGAATCTGGTCGGAAAAGGAGGGTTTGAAATGTGTATAAAGGTTGTC'TTCAT  
GATGGAAGTATCATCGCGGTGAAGAGATTAAAGGATATAAACAATGGTGGTGGAGAGGTT  
CAGTTTCAGACAGAGCTTGAAATGATAAGCCTTGCCGTCCACCGGAATCTCCTCCGCTTA  
TACGGTTTCTGTACTACTTCTCTGAACGGCTTCTCGTTTATCCTTACATGTCCAATGGC  
30 AGTGTGCTTCTCGTCTCAAAGCTAAACCGGTATTGGATTGGGGCACAAAGAAAGCGAATA  
GCATTAGGAGCAGGAAGAGGGTTGCTGTATTGTCATGAGCAATGTGATCCAAAGATCATT  
CACCGTGATGTCAAAGCTGCGAACATACTTCTTGACGATTACTTTGAAGCTGTTGTGCGGA  
GATTCGGGTTGGCTAAGCTTTTGGATCATGAGGAGTCGCATGTGACAACCGCCGTGAGA  
GGAACAGTGGGTCACATTGCACCTGAGTATCTCTCAACAGGACAATCTTCTGAGAAGACA  
35 GATGTGTTGCGTTTCGGGATTCTTCTCTCGAATTGATTACTGGATTGAGAGCTCTTGAA  
TTCGAAAAGCAGCAAAACCAAGAGGAGCGATACTTGATTGGGTAAAGAACTACAACAA  
GAGAAGAAGCTAGAACAGATAGTAGACAAGGATTTGAAGAGCAACTACGATAGAATAGAA  
GTGAAGAAATGGTTCAAGTGGCTTTGCTTTGTACACAGTATCTTCCCATTCACCGTCCT  
AAGATGTCTGAAGTTGTGAGAATGCTTGAAGGCGATGGTCTTGTGAGAAATGGGAAGCT  
40 TCTTCTCAGAGAGCAGAAACCAATAGAAGTTACAGTAAACCTAACGAGTTTTCTTCCTCT

GAACGTTATTTCGGATCTTACAGATGATTCCTCGGTGCTGGTTCAAGCCATGGAGTTATCA  
GGTCCAAGATGAcaagagaaactatatgaatggctttgggtttgtaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS14 protein.

Different domains are spaced and shown from the N-terminus  
towards the C-terminus. Overall domain structure is similar as  
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain  
represents a signal sequence. The second domain contains a  
leucine zipper motif, containing 3 leucine residues, each  
separated by seven other amino acids. The third domain  
15 contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich  
repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain  
contains many serine and proline residues, and is likely to  
20 contain hydroxy-proline residues, and to be a site for O-  
glycosylation. The sixth domain contains a single  
transmembrane domain after which the predicted intracellular  
domains are positioned. The seventh domain has an unknown  
function. The eighth domain represents a serine / threonine  
25 protein kinase domain (Schmidt et al. 1997) and is probably  
also containing sequences for protein / protein interactions.  
The ninth domain has an unknown function. The last and tenth  
domain at the C-terminal end represents part of a single  
leucine rich repeat, probably involved in protein / protein  
30 interactions.

MLQGRREAKKSYALFSSTFF  
FFFICFLSSSSAELTDKV

35 VALIGIKSSLTDP  
HGVL MNWDDTAVD

PCSWNMITCSDGFVIR

LEAPSQNLSGTLSS  
SIGNLTNLQTVYRLLQNNYITGNI  
PHEIGKLMKLKTLDDLSTNNFTGQI  
5 PFTLSYSKNLHRRV NNNSLTGTI  
PSSLANMTQLTFDLDSYNNLSGPV  
PRSLAKTFNVMGNSQICPT  
  
GTEKDCNGTQPKMSITLNSSQR  
10 TKNRK  
  
IAVVEGVSLTCVCLLIIGFGFLLWW  
  
RRRHNKQVLFFDINEQNKE  
15 EMCLGNLRRFNFKELQSAT  
  
SNFSSKNLVGKGGFGNVYKGCLHD  
GSIIAVKRLKDINNGGGEVQFQ  
TELEMISLAVHRNLLRLYGECT  
20 TSERLLVYPYMSNGSVA  
SRLKAKPVLWDGTRKRIALGAG  
RGLLYLHEQCDPKIIHRDVKAA  
NILLDDYFEAVVGDFGLAKLLD  
HEESHVTTAVRGTVGHIAPEYL  
25 STGQSSEKTDVFGFGILLLELI  
TGLRALEFGKAANQRGAILDW  
VKKLQQEKKLEQIVDKDLKSNY  
DRIEVEEMVQVALLCTQYLPFH  
RPMSEVVRMLE  
30 GDGLVEKWEASSQRAET  
NRSYSKPNEFSSS  
  
ERYSDLTDDSSVLVQAMELSGPR  
35

## Legends

## Figure 1

5

The different domains of the predicted RKS gene product have the following functions:

The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in  
10 targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein  
15 protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and  
20 Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine /. proline rich region. The next domain displays all the characteristics of a single transmembrane  
25 domain (<http://genome.cbs.dtu.dk/services/TMHMM/>). At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain  
30 with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

## Figure 2

35

Alagnumt of the predicted protein sequences of the different RKS gene products from *Arabidopsis thaliana* with alignX, Vector NTI Suite 5.5 resulted in a phylogenetic tree in which

the relative homology between the different RKS members is shown.

Figure 3

- 5 Intron-Exon boundaries of the genomic regions on the chromosomes of *Arabidopsis thaliana* encoding the different RKS gene products. Exons are shown as boxes, whereas intron sequences are shown as lines. Sequences encoding LRR domains are displayed in gray colour, transmembrane regions in black.

10

Figure 4.

Cromosomal location of RKS genes in *Arabidopsis thaliana*, showing colocalisation with GASA genes.

- 15 Figure 5. A signaling complex comprising molecules of RKS proteins, ELS proteins, NDR/NHL proteins and SBP/SPL proteins.

Figure 6.

- Second generation (T2) tobacco seedlings germinated on MS medium. Transformations were performed with DNA clone 2212-15, representing the overexpression construct GT-RKS4-s. T2 seedlings derived from T1 plant 15.7 shows co-suppression effects while T1 plant 15.6 shows no obvious changes in level of RKS4. T1 plants 15.9 and 15.3 show overexpression effects.
- 20
- 25 Plant 15.7 has the lowest remaining level of RKS4 gene product, whereas plant 15.3 has the highest level of RKS4 gene product.

Figure 7

- 30 Second generation (T2) tobacco plants. In the upper row the offspring from a co-suppressing T1 plant 15.7 is shown. The middle row shows plants derived from a transgenic T1 plant 15.6 with no clear changes in level of RKS4 is shown while the bottom row shows plants derived from a T1 plant 15.3 in which
- 35 the levels of RKS4 are increased by the introduction of the overexpression construct GT-RKS4-s.

## Figure 8

Second generation (T2) tobacco plants. Plants derived from a co-suppressing T1 plant 15.7 show a reduction in plant size and a delay in the initiation and outgrowth of primordia. The control empty vector transgenic plants show no visible differences in growth compared with the offspring from the transgenic 15.6 plant, in which the endogenous level of RKS4 gene product was not changed. In the overexpressing plants 15.9 and 15.3 organ size was increased, similar as the number of initiated leaf primordia.

## Figure 9

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS4 gene product is decreased (right picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia is decreased in the transgenic antisense plant compared with the wildtype control.

## Figure 10.

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS4 gene product is decreased (bottom left picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The upper right picture shows a wildtype flower of the same age as the transgenic antisense flower, grown under similar growth conditions. Total flower size is only slightly decreased in the transgenic antisense flower compared with the control flower, whereas organ size of petals is strongly decreased.

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS4 gene product is increased (upper left picture) due to the presence of a transgenic RKS4 overexpressing construct (GT-RKS4-6s). Compared with the wildtype control flower, total flower size of the transgenic flower is clearly increased. Both sepal and petal organ size is clearly increased compared

with the control.

For comparison an *Arabidopsis thaliana* WS plant is shown which has been transformed with a construct encoding the GAS3 gene in sense direction, i.e. overexpressing GAS3.

5

Figure 11.

Formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS plants under influence of overexpression of RKS4.

- 10 RKS4 overexpression results in increases in flower and seed organ size that could be due to increase in cell elongation and/or cell division. In order to analyse the cell division patterns in plants with deregulated RKS4 expression the mitotic activity in transgenic plants was analyzed with the a
- 15 unstable GUS reporter under the control of a cyclin B1;1 promoter (the Plant Journal 1999 (4) 503-508 Spatio-temporal analysis of mitotic activity with a labile cyclin-GUS fusion protein). *Arabidopsis thaliana* WS seedlings with the pCDG construct did not show gus activity (cell division) in
- 20 hypocotyls (top) whereas the same pCDG line crossed with a constitutive RKS4 construct showed mitotic activity as indicated by GUS-positive cells (bottom); indicating that RKS4 overexpression activated mitotic activity in hypocotyls.

25 

Figure 12

In *Arabidopsis thaliana* WS, the seed size is influenced by changing levels of RKS4 gene product. Constitutive overexpression of RKS4 results in increases in seed size (left) compared with control wildtype seeds (right). Antisense

30 constitutive expression of RKS4 cDNA (middle) results in a decrease in seed size compared with the control (right). Magnification is identical in all photos as shown by the bar size.

35

Figure 13

Organ size can be influenced by either modulating cell division or cell elongation or a combination of both. In order to identify the total number of cells and the cell size within an organ the apical site of petals of mature *Arabidopsis* flowers was investigated. Petal organ size is clearly influenced by modulation of RKS4 gene product levels (bottom row for the flowers from which the apical petal epidermal cells were identified ). Epidermal cell size is not changed in transgenic plants compared with the control.

10

Figure 14

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS10 gene product is increased (right picture) due to the presence of a transgenic RKS10 overexpressing construct. The left picture shows the apical epidermus of a full grown cotyl from an empty vector transgenic seedling of the same age as the transgenic overexpressing cotyl, grown under similar growth conditions..

20 

Figure 15

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS10 gene product is decreased (right picture) due to the presence of a RKS10 antisense construct The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia remains similar in both the transgenic antisense plants and the wildtype control.

30 

Figure 16

In order to determine organ size variations in transgenic RKS10 transgenic plants compared with empty vector control transgenic plants (pGreen4K), flower organ size was determined of the four open flower stages of *Arabidopsis* inflorescences. The four successive flower stages are photographed under similar magnifications. No obvious changes in organ length could be observed in size of sepals, petals, stamen and carpel

between empty vector control flowers (pGreen4K), flowers with an antisense RKS10 construct (a) or plants overexpressing the RKS10 cDNA under the control of a 35S promoter (S

5 Figure 17

Tissue cultured auxin treated *transgenic Arabidopsis* T2 seedlings were grown on MS agar plates without hormones for a period of 3 weeks. Regeneration potential was scored and the formation and outgrowth of multiple shoot apical meristems from single seedling origin was displayed as (+). The formation and outgrowth of only one shoot apical meristem, leading to the formation of a normal rosette of leaves from individual plants was displayed as (-). Positive regeneration controls consisted of seedlings overexpressing either KNAT1, CUC2, IPT or cycD3. All of these showed an increase of regeneration capacity (+) compared with a negative control GUS overexpressing plant pGreen5K (-). Representative examples of RKS and ELS cDNA overexpressing (s) or antisense (a) cosuppressing constructs in transgenic plants are shown in the bottom panels.

Figure 18.

Tobacco leaf discs were stably transformed with the RKS0 overexpressing construct GT-RKS0-23S and from a single transformation event, large numbers of regeneration plantlets were isolated and subcultured. All of the regenerated plants were potted and flowered. The original transformation event could be kept continuously in tissue culture indefinitely.

30 Figure 19

Seedlings from *transgenic Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen5K, overexpressing the GUS gene) in which fasciation could never be observed.

## Figure 20 - 23

Primary root tips of transgenic *Arabidopsis* plants (top rows) photographed under similar magnification. The bottom rows show the corresponding seedlings (also between each other under the same magnification). Figure 23 shows the specific *Arabidopsis* transgenes with a strong increase in root outgrowth.

## Figure 24

Average root length of 10-30 transgenic *Arabidopsis* T2 seedlings from one T1 transgenic plant is shown.

## Figure 25

T3 seedlings are shown from a strong co-suppressing RKS10 antisense construct line (T1-4; T2-6; T3 generation) and a strong overexpressing line (T1-4; T2-6; T3 generation). The overexpressing line is different and stronger from the one shown in Figure 4.1-4.5. Pictures are taken under similar magnifications.

20

## Figure 26

T2 seed was germinated on horizontal MS agar plates and pictures were taken under similar magnification of representative examples of the lateral root development from transgenic RKS and ELS transgenic roots.

25

## Figure 27

Pictures taken from transgenic RKS8 or RKS10 overexpressing roots taken directly behind the tip zone. Pictures are taken under same magnification.

30

## Figure 28

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS or ELS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K).

35

Overexpression of RKS10 and ELS1 (S) and cosuppression with antisense constructs of RKS8 and also RKS10, result in increased numbers of developing generative meristems. The generative shoots are photographed with similar magnification.

#### Figure 29

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K). The top panel shows adult plants under similar magnification. Compared with the control, RKS10 overexpression results in an extreme bushy phenotypic plant. The results of co-suppressing the RKS8 gene product are less dramatic with respect to the bushiness. However, also in these transgenic plants the number of generative meristems is strongly increased compared with the control. The bottom panel shows the generative shoot in detail under similar magnification.

#### Figure 30

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in transgenic *Arabidopsis* plants containing an antisense (a) RKS10 construct. The terminal flower meristem produces 2 sepals, 1 petal, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. Two new flowers are protruding from this structure, containing all flower organs in normal numbers.

#### Figure 31

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in transgenic *Arabidopsis* plants T1-11 containing an antisense (a) RKS10 construct. The

terminal flower meristem produces 1 sepal, 2 petals, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. An undetermined  
5 flower meristem is protruding from the open carpel structure and forms a number of new flowers, including normal flowers (right) and another abnormal flower (left) which consists of a flower with half of the sepal, petal and stamen organs formed and a new terminal flower meristem protruding from this  
10 structure, developing in structures as seen in Figure 7.5. The stamen contain only small numbers of (viable) pollen compared with wildtype stamen (see also chapter 5).

Figure 32

15 Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-11 containing an antisense (a) RKS10 construct (overview shown in Figure 7.4). The terminal flower meristem  
20 produces half the normal number of sepals, petals and stamen. The remaining part of the flower structure has converted into a new structure containing a new stem containing a single organ structure resembling a fusion between a petal and a sepal. On this structure several (viable) pollen grains can be  
25 observed.

Figure 33

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in a transgenic *Arabidopsis*  
30 plant T1-12 containing an antisense (a) RKS10 construct. The terminal flower meristem originating from an undetermined generative meristem is here producing an axillary secondary undetermined meristem (left picture), a single organ resembling a stamen (bottom left), a normal flower and a  
35 terminal flower. This terminal flower structure contains 2 normal sepals, 2 normal petals, 2 normal stamen (with only a few viable pollen) and two organs resembling a fusion of

sepals /petals/stamen (see also figure 7.7). From this terminal flower structure two new flowers emerge (in a similar fashion as observed in Figure 7.3) containing normal numbers of flower organs (right photos). At the top of this figure a control inflorescence is shown schematically with terminal flower meristems as normally originate from the generative *Arabidopsis thaliana* generative meristem.

#### Figure 34

Schematic drawing and detailed pictures of several of the structures as shown in figure 7.6. At the right the organs resembling a fusion between sepals/petals/stamen are shown with viable pollen sticking out from these structures. At the top left the single stamen-like organ directly protruding from the main stem is shown.

#### Figure 35

Transgenic *Arabidopsis* plants overexpressing the RKS13 gene product show a modification of the normal flower inflorescence architecture, somewhat resembling the structures observed in RKS10 antisense plants. A terminal flower containing a normal seed developing silique and a small number of sepals, petals and stamen, develops at least 4 additional terminal flower meristems that develop abnormally themselves, resulting in open carpel structures and modifications of organ structures.

#### Figure 36

Transgenic plants in which the RKS and / or ELS genes are introduced behind a constitutive 35S promoter in an overexpressing (S) or antisense (a) configuration are analyzed for sterility and characterized further for defects in proper pollen development. As a negative control the normal pollen development of a transgene containing the empty expression vector (pG4K) was included. First generation transgenic flowers of RKS10 expressing constructs and second generation control vector and ELS2 are shown under similar magnification. In detail the stigmatic surface and surrounding stamen, are

shown under similar magnification, showing the presence or absence of pollen on the stamen or the stigmatic surface.

## Detailed description

**1. Modifying organ size**

5

Plant size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase:

- the size of plant organs
- the growth rate
- the yield of harvested crop
- the yield of total plant material
- the total plant size

Decreasing the levels of endogenous RKS gene product is provided in order to decrease:

- the size of plant organs

the growth rate  
the total plant size

5

**Results obtained (see also figures 6 to 13)**

Overexpression and antisense constructs of full length RKS  
cDNA clones have been made under the control of 35S  
promoters. Transgenic plants have been produced in *Arabidopsis*  
10 *thaliana* and in *Nicotiana tabacum*. Subsequent generations of  
stably transformed plants were investigated for phenotypes and  
analyzed in detail. The phenotype observed in transgenic  
plants with antisense constructs of RKS4 (GT-RKS4-a) could be  
described as dwarf plants in which all plant organs showed a  
15 decrease in organs size and growth rate. Overexpression of  
RKS4 (GT-RKS4-s) resulted in plants with increased size of  
organs and an increase in growth rate. Since cell size alone  
was not responsible for the modifications in organ size of  
petals it can be concluded that RKS4 is involved in the  
20 regulation of the cellular divisions during plant growth and  
organ formation. Overexpression of RKS 4 results in an  
increase of cellular divisions whereas a decrease in  
endogenous RKS 4 gene product levels within the plant results  
in a decrease of cellular division rates.

25

**Literature**

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## 2. Cell division

The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes, especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

### 30 Possible Applications

Elevation of the levels of the regulating RKS signaling complex members in plant cells in order to increase:  
the size of plant organs  
the growth rate  
35 the yield of harvested crop  
the yield of total plant material  
the total plant size

- Decreasing the levels of endogenous RKS signaling complex members in order to decrease:  
the size of plant organs  
5 the growth rate  
the total plant size

#### Results obtained

- Overexpression and antisense constructs of full length RKS  
10 cDNA clones have been made under the control of 35S  
promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
- 15 Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division. Another example of RKS genes involved in cellular proliferation is provided by RKS10. Overexpression of RKS10  
20 (S) results in a decrease in apical epidermal cells (Figure 14) compared with control plants containing an empty expression cassette (pGreen4K). Co-suppressing the endogenous RKS 10 gene in plants containing an antisense construct (a) showed clearly larger epidermal cells as the corresponding  
25 cells in wildtype control plants (Figure 15). In contrast to the plant phenotypes shown in RKS4 transgenic plants, no differences in plant or organ size could be observed in the RKS10 transgenic plants or organs. This shows that although the organ size remains constant, the number of cells within  
30 these organs is variable due to the differences in size of individual cells. These results indicate that normal RKS4 function within the plant can be described as an activator of cellular division.
- Normal RKS10 function also involves an activation process on  
35 cellular division rate. This effect is also detectable in the root in the region directly behind the tip zone, where in the RKS10 overexpressing transgenes cellular divisions were

detectable in a region where normally cell proliferation has ceased. The plane of divisions of root cells in these transgenes is also clearly different from the normal plane of root cell division, resulting in clumps of cells with all

5 types of division planes possible.

In contrast to RKS4, the final organ size in RKS10 transgenic plants is under the control of other organ size restriction processes, in such a way that the final organ volume remains constant (Figure 16). RKS4 and RKS10 are essentially involved  
10 in the same cell cycle activation process, but either addition organ size controlling functions of these RKS genes or the hierarchical order in which they regulate the cell cycle is different.

15

#### Literature

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### 3. Regeneration

Modification the levels of different RKS and ELS genes within  
5 plants allows the initiation and / or outgrowth of apical  
meristems, resulting in the formation of large numbers of  
plantlets from a single source. A number of gene products that  
is able to increase the regeneration potential of plants is  
known already. Examples of these are KNAT1, cycD3, CUC2 and  
10 IPT. Here we show that modulation of the endogenous levels of  
RKS genes results in the formation of new shoots and plantlets  
in different plant species like *Nicotiana tabacum* and  
*Arabidopsis thaliana*. herewith the invention provides a method  
for modulating a developmental pathway of a plant or plant  
15 cell comprising modifying a gene or modifying expression of  
said gene, wherein said gene is encoding a protein belonging  
to a signaling complex comprising RKS protein, ELS protein,  
NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein,  
allowing modulating apical meristem formation, in particular  
20 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or  
RKS10 gene or functional equivalent thereof. A direct  
application of a method according to the invention is the  
stable or transient expression of RKS and ELS genes or gene  
products in order to initiate vegetative reproduction.  
25 Regeneration can be induced after overexpression of for  
example RKS0 and ELS1; or by co-suppression of for example the  
endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or  
co-suppression of these RKS and ELS gene products can be  
either transient, or stable by integration of the  
30 corresponding expression cassettes in the plant genome.

### Results obtained

Overexpression and antisense constructs of full length RKS and  
ELS cDNA clones have been made under the control of 35S  
35 promoters. Transgenic plants have been produced in *Arabidopsis*  
*thaliana* and in *Nicotiana tabacum*. Subsequent generations of

stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated in liquid MS medium supplemented with 1 mg/L 2,4-D for 1 week, followed by extensive washing and plating of the seedlings onto MS agar plates without hormones. Control transgenic seedstocks containing either a negative control vector (pGreen5K); or positive control overexpression constructs of gene products known to increase the regeneration potential (IPT, KNAT1, CUC2 and cycD3) were characterized for regeneration potential together with seedstocks from plants either overexpressing (s) or co-suppressing (a) all RKS and ELS gene products (Figure 17). Overexpression of the ELS1 and RKS0 cDNA clones resulted in an increase of shoot apical meristem formation and outgrowth, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only increased regeneration results are shown). Antisense constructs of RKS3, RKS4, RKS8 and RKS10 also resulted in an increased formation and outgrowth of apical meristems (Figure 17).

T1 generation *Nicotiana tabacum* tissue cultures transformed with ELS and RKS gene products in either overexpression (s) cassettes or antisense co-suppression (a) cassettes allowed the regeneration of indefinite number of offspring plants from a single transformed cell origin (Figure 18). An example is shown for the overexpression of the GT-RKS0-23S construct. The resulting plants obtained from one transformation event in general showed no phenotypes. Only a subset of plants displayed RKS0 overexpression phenotypes (like loss of apical dominance and early flowering).

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#### 4. Fasciation

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs.

Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems as shown in Figure 19. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type (an example is shown in Figure 19 where the fasciated meristem of a RKS0-7S *Arabidopsis* plant in which endogenous RKS0 gene product

levels have been deregulated clearly terminates in an *Umbelliferae* type inflorescence.

#### Results obtained

- 5 Overexpression and antisense constructs of full length RKS  
cDNA clones have been made under the control of 35S  
promoters. Transgenic plants have been produced in *Arabidopsis*  
*thaliana*. Subsequent generations of stably transformed plants  
were investigated for phenotypes and analyzed in detail.
- 10 T2 transgenic seedlings of *Arabidopsis* were germinated on MS  
agar plates without hormones. Control transgenic seedstocks  
containing a negative control vector (pGreen5K) were tested  
for their ability to induce fasciation (Overexpression  
constructs (s) of RKS0, RKS8 and RKS10 cDNA clones resulted in  
15 fasciated plants, whereas antisense constructs (a) of these  
cDNA clones did not increase the regeneration potential (only  
positive results are shown). Antisense constructs of RKS3  
gave also rise to fasciation (Figure 19).

20

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## 5. Root development

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of the RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6 RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant

hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or  
5 ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the  
10 contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

#### Results obtained

15 Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.  
20 T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector pGreen4K (empty expression vector) and / or pGreen5K (a GUS overproducing vector) were included as references for normal root  
25 development. Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in  
30 which fasciation could be routinely observed are shown together with a negative control plant (pGreen4K, containing an expressing cassette without an insert cDNA). Seedlings are germinated and grown on vertically placed MS agar plates.

35

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## 6. Apical meristems

All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated  
5 early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem  
10 formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The  
15 invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and  
20 RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and /  
25 or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an  
30 undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

35 Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows

the formation of completely new types of flowers and fused fruit structures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression  
5 results in an extremely bushy phenotype.

### Results obtained

Changing the normal levels of endogenous RKS10 within the  
10 plant, either by overexpressing or co-suppressing the RKS10 cDNA, results in an increase in generative meristem development (Figure 28).

Compared with the control empty vector transgenic pGreen4K plants, large number of meristems are initiated at places were  
15 normally no meristems initiate and / or develop. A clear example is shown by co-suppressing the RKS8 gene (Figure 29), where many new inflorescence meristems are initiated from the central generative meristem compared with control pGreen4K plants of the same age. This phenotype is even more extreme in  
20 RKS10 overexpressing plants where the resulting plants are extremely bushy with very large numbers of generative meristems formed. Inactivation of the endogenous RKS10 gene in *Arabidopsis* results in modification of meristematic identity as can be shown in Figure 30. A determined flower meristem  
25 develops into two new normal terminal flower meristems and a number of terminal flower organ primordia. Another example is shown in Figure 31 where meristem determination is switched from a terminal flower meristem, that normally result only in the normal numbers of terminal organ primordia, towards a  
30 number of organ primordia, a new undetermined generative meristem that develop into normal flowers or in a new terminal flower meristem with developmental abnormalities. Only half of the terminal flower primordia develop normally while an extra structure arises resembling a new flower stem with a  
35 petal/stamen like organ. The few pollen detectable on this structure (Figure 32) were able to pollinate a MS1 (male sterile) *Arabidopsis* flower. Figure 33 shows the meristematic

developmental switch from a terminal flower meristem into a new undetermined generative meristem, that gives rise to a new formation of another undetermined meristem, and several normal and abnormal terminal flowers. The abnormal flowers again show the fusion of different structures, in this case from sepals, petals and stamen together (Figure 34). Surprisingly, directly on the generative stem another structure, resembling a single stamen was detectable. All these data indicate that a decrease in RKS1 expression levels results in switches in the meristematic identity. Meristems can switch forward and backward between developmental stages, indicating that RKS10 is normally involved in regulating the meristematic identity and the developmental order of meristematic development. RKS13 seems to be involved in similar processes, as can be concluded from the switches in flower meristematic outgrowths observed in figure 35. Modification of the expression levels of RKS1 also results in modified meristem identity. Suppression of endogenous RKS1 levels results in a developmental switching of generative meristems towards vegetative meristems, together with other phenotypes (results not shown).

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## 7. Male sterility

Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

### 30 Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic plants

containing a negative control vector pGreen4K (empty expression vector) were included as references for normal stamen and pollen development. RKS10 and ELS2 resulted in sterile plants when overexpressed in *Arabidopsis*. Antisense RKS10 plants resulted in a strong reduction in the number of pollen formed (Figure 36). In order to determine whether pollen development itself was the reason for sterility (and not a combination of pollen developmental mutants coupled to either embryo lethals or female gametogenesis defects), reciprocal crosses were performed between sterile transgenic plants and wildtype *Arabidopsis thaliana* WS plants. These results confirmed that the sterile plants with overexpressing RKS10 and ELS2 constructs were male sterile but completely female fertile. No defects could be observed in embryo development from crosses between female transgenic overexpressors and male wildtype pollen (results not shown). Since both antisense and overexpressing constructs of the RKS10 gene showed defects in proper pollen development we conclude that normal levels of endogenous RKS10 gene product are essential for proper pollen formation, outgrowth and differentiation. In the ELS2 overexpressing plants the initiation of pollen grains was not inhibited. However the proper development of pollen grains in full grown viable pollen was clearly inhibited .

25

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35

## 8. Resistance mechanisms

Two-hybrid interaction experiments have already shown *in vitro* interaction between RKS and NDR0-NHL and members of the SBP/SPL family. Here we show that *in vivo* the individual components of this signalling cascade are regulating identical processes, as based on functional genomics on transgenics plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex.

Here we show a large number of new members of the NDR/NHL gene family and we postulate a function as syntaxins in the pathogen resistance:

15 **At2g27080;**  
 MAERVYPADS PPQSGQFSGN FSSGEFPKKP APPPSTYVIQ VPKDQIYRIP PPENAHRFEQ  
 LSRKKTNRSN CRCCFCSFLA AVFILIVLAG ISFAVLYLIY RPEAPKYSIE GFSVSGINLN  
 STSPISPSFN VTVRSRNGNG KIGVYYEKES SVDVYYNDVD ISNGVMPVIFY QPAKNVTVVK  
 LVLSGSKIQL TSGMRKEMRN EVSKKTVPFK LKIKAPVKIK FGSVKTWTMI VNVD CDVTVD  
 20 KLTAPSRIVS RKCSHDVDLW \*\*

**At5g21130**  
 MTVEKPQEMT GDTNSDGFLT NKDVHRIKHP SLDTNDSSSS RYSVDSQKSR IGPPPGTYVI  
 KLPKDQIYRV PPPENAHRYE YLSRRKTNKS  
 25 CCRRCLCYSL SALLIIIVLA AIAFGFFYL  
 YQPHKPQFSV SGVSVTGINL TSSSPFSPVI RIKLRSQNVK GKLGLIYEKG NEADVFFNGT  
 KLGNGEFTAF KQPAGNVTVI VTLVKGSSVK LKSSSRKELT ESQKKGKVPF GLRIKAPVKF  
 KVGSVTTWTM TITVDCKITV DKLTASATVK TENCETGLSL L\*

30 **At1g65690**  
 MSQHQQIYPV QDPEAATARP TAPLVPRGSS RSEHGDPKSV PLNQRQRFV PLAPPKKRRS  
 CCCRCFCYTF CFLLLLVAV GASIGILYLV FKPKLPDYSI DRLQLTRFAL NQDSSLTTAF  
 NVTITAKNPV EKIGIYYEDG SKITVWYMEH QLSNGSLPKF YQGHENTTVI YVENTGQTQN  
 ASGLRTTLEE QQRTGNIPL RIRVNQVVRV KFGKLKLFV RFLVRCGVFV DSLATNNVIK  
 35 IQSSSCKFRL RL\*

**At5g36970**  
 MSDHQKIHPV SDPEAPPHT APLVPRGSSR SEHGDPTKTQ QAAPLDPPRE KKGSR  
 CWCRCVCYTLLVLF LLIVIVGAIV GILYLVFRPK FPDYNIDRLQ LTRFQLNQDL  
 40 SLSTAFNVTI  
 TAKNPNEKIG IYYEDGSKIS VLYMQTRISN GSLPKFYQGH ENTTIILVEM TGFTQNATSL  
 MTTLQEQQL TGSIPLRIRV TQPVRILKLG LKLMKVRFLV RCGVSVDLSA ANSVIRVRSS  
 NCKYRFRL\*

45 **At1g54540**  
 MGDQKIHVP LQMEANKTKT TTPAPGKTVL LPVQRPIPPP VIPSKNRNMC CKIFCWVLSL  
 LVIALIALAI AVAVVYFVPH PKLPSYEVNS LRVTNLGINL DLSLSAEFKV EITARNPNEK  
 IGIYYEKGSH IGWYDKTKL CEGPIPRFYQ GHRNVTKLV ALTGRAQYGN TVLAALQOQQ  
 QTGRVPLDLK VNAPVAIKLG NLKMKKIRIL GSCKLVVDSL STNNNINIK SDCSFKAKL\*  
 50

**At5g06320**

MADLNGAYYG PSIPPPKKVS HSHGRRGGGC GCLGDCLGCC GCCILSVIFN ILITIAVLLG  
IAALIIWLIF RPNAIKFHVT DAKLTEFTLD PTNNLRYNLD LNFTIRNPNR RIGVYDEIE  
VRGYYGDQRF GMSNNISKFY QGHKNTTVVG TKLVGQQLVL LDGGERKDLN EDVNSQIYRI  
DAKLRLKIRF KFGLIKSWRF KPKIKCDLKV PLTSNSTSGF VFQPTKCDVD F\*\*

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**At5g11890**

MTDRVFPASK PPTATNGAPP VGSIPPPAP ATVTSNGTTN GMANQKPQVY IPANRPVYRP  
QPYSRRHHHQ SRPSCRRICC CCCFWSILII LILALMTAIA ATAMYVIYHP RPPSFVPSI  
RISRVLNLTTS SDSSVSHLSS FNFNLTISEN PNQHLFSYD PFTVTVNSAK SGTMLGNQTV  
10 PAFFSDNGNK TSFHGVIATS TAARELDPDE AKHLRSDLTR ARVGYEIEMR TKVKMINGKL  
KSEGVBIKVT CEGFEGTIPK GKTPIVATSK KTKCKSDLSV KVKWWSF\*

**At1g17620**

MTDDRVPYAS KPPAIVGGGA PTTNPTFPAN KAQLYNANRP AYRPPAGRRR TSHTRG  
15 CCCRCCCWTIFVII LLLLIVAAAS AVVYLIYRPQ RPSFTVSELK ISTLNFTSAV  
RLTTAISLSV  
IARNPNKNVG FIYDVTIDITL YKASTGGDDD VVIGKGTIAA FSHGKKNTTT LRSTIGSPPD  
ELDEISAGKL KGDLLAKKAV AIKIVLNSKV KVKMGALKTP KSGIRVTCEG IKVVAPTGGK  
ATTATTSAAK CKVDPRFKIW KITF\*\*

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**At3g11650**

MGSKQPYLNG AYYGPSIPPP PKAHRSYNSP GFGCCCFSCS GSCLRCCGCC ILSLICNILI  
AVAVILGVAA LILWLIFRPN AVKPYVADAN LNRFSFDPNN NLHYSLDLNF TIRNPNQVRG  
25 VYDEFVSUGS YYGDKRFGSA NVSSFYQGHK NTTVILTKE GQNLVVLGDG ARTDLKDEK  
SGIYRINAKL RLSVRPKFWF IKSWKLLPKI KCDDLKIPLG SSNSTGGGKF QPVQCDFDLS\*\*

**At2g22180**

MEGPRRPPSA TAPDSDDDKP DDPPSVWHRP TSSLPALPSL DPPSHGSHHW RNHSLNLSPL  
30 PTTSSPPLPP PDSIPELETY VVQVPRDQVY WTPPPEHAKY VEKRSKNPEK NKKKGCSKRL  
LWFFIILVIF GFLLGAILLI LHFAFNPTLP VFAVERLTVN PSNFEVTLRA ENPTSNMGVR  
YMEKNGVVS LTYKNKSLGS GKFFGLSQAA SGSDKVNKVL NGSTKNAVVO PRGSKQPVVL  
MLNMLKAEY BAGPVKRNKE VVVTCDVKVK GLLDKAKVEI VSENCESEFK N\*

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**At5g22870**

MCHKPKLELM PMETSPAQPL RRPSLICYIF LVILTILFMA AVGFLITWLE TKPKKLYRTV  
ENASVQNFNL TNDNHMSATF QFTIQSHNPN HRISVYSSV EIFVKFKDQT LAFDTVEPFH  
QPRMNVKQID ETLIAENVAV SKSNGKDLRS QNSLGKIGFE VFVKARVRFK VGIWKSSHRT  
40 AKIKCSHVTV SLSQPNKSQN SSCDADI\*

**At2g35980**

MAABQPLNGA FYGSPVPPPA PKGYRRGHG RGC GCCLLSL FVKVIISLIV ILGVAALIFW  
LIVRPRAIKF HVTDASLTRF DHTSPDNILR YNLALTVPVR NPNKRIGLYY DRIEHAHAYE  
GKRFTSTILT PFYQGHKNTT VLTPTFQGGN LVIFNAGQSR TLNAERISGV YNIBIKFRLR  
45 VRFKLGDLKF RRIKPKVDCD DLRLPLSTSN GTTTTSTVFP IKCDFDF\*\*

**At2g46300**

MADYQMNPEVL QKPPGYRDPN MSSPPPPPPP IQQQPMRKAV PMPTSYPKK KRRSCCRFCC  
CCICITLVLF IFLLLVGTAV FYLWFDPKLP TFSLSAFRLD GFKLADDPDG ASLSATAVAR  
50 VEMKNPNKSL VFYNGNTAVD LSVGSGNDET GMGETTMNGF RQGPKNSTSV KVETTVKNQL  
VERGLAKRLA AKFQSKDLVI NVVAKTKVGL GVGGIKIGML AVNLRCCGVS LNKLDTDSPK  
CILNTLKWKYK IISN\*

**At4g05220**

155 MTPDRRTIPI RTSPVPRAQP MKRHHSASY AHRVRESLST RISKFICAMF  
LLVLEFFVGVI AFILWLSLRP HRPRFHIQDF

VVQGLDQPTG VENARIAFNV TILNPNQHMG VYFDSMEGSI YYKDQRVGLI  
 PLLNPFQOP TTTTIVTGTL TGASLTVNSN RWTEFSNDRA QGTVGFRLLDI  
 VSTIRFKLHR WISKHHRMHA NCNIVVGRDG LILPKFNHHR CPVYFT\*

## 5 At2g35460

MANGLNGASY GPPIKPPVKT YYSHGRRGSD VCGICGCFS SCLCCGGCL VNIICNILIG  
 VLVCLGVVAL ILWFILRPNV VKFQVTEADL TRFEFDPRSH NLHYNISLNF SIRNPNQRLG  
 IHYDQLEVRG YYGDQRFSA NMTSFYQGHK NTTVVGTELN GQKLVLGAG GRRDFREDRR  
 SGVYRIDVKL RFKLRPFKGF LNSWAVRPKI KCHLKVPLST SSSDERFQFH PTKCHVDL\*

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## At2g27260

MQDPSRPATG YPYPPYPNP QQQQPPTNGY PNPAAGTAYP YQNHNPYYAP QPNPRAVIIR  
 RLFIIVFTTFL LLLGLILFIF FLIVRPQLPD VNLNSLSVSN FNVSNQVSG KWDLQLQFRN  
 PNSKMSLHYE TALCAMYNR VSLSETRLQP FDQGGKQTV VNATLSVSGT YVDGRLVDSI  
 15 GKERSVKGNV EFDLRMISYV TFRYGAFRRR RYVTVYCDDV AVGVVPVSSGE GKMVGSSKRC  
 KTY\*\*

## At4g01410

20 MGEGEAKAEH AAKADHKNA SASSTPESYS KEGGGGGGDA RRAICGAIFT ILVILGIIAL  
 ILWLVIYRPHK PRLTVVGA AI YDLNFTAPPL ISTSVQFSVL ARNPNRRVSI HYDKLSMYVT  
 YKQIITPPL PLPPLRLGHK STVVIAPVMG GNGIPVSPEV ANGLKNDEAY GVVLMRVVIF  
 GRLRWKAGAI KTGRYGFYAR CDVWLRFPNS SNGQVPLLAP STCKVDV\*

## At5g22200

25 MTGRYCDQHN GYEERRMRMM MRRIAWACLG LIVAVAFVVF LVWAILHPHG PRFVLQDVTTI  
 NDFNVSQPNF LSSNLQVTVS SRNPNDKIGI FYDRLDIYVT YRNQEVTLAR LLPSTYQGHL  
 EVTWVSPFLI GSAVPVAPYL SSALNEDLFA GLVLLNIKID GWVRWKVGSW VSGSYRLHVN  
 CPAFITVTGK LTGTGPAIKY QLVQRCADV \*

## 30 At1g61760

MHNKVDLSPV RSNPSTRPIS RHHSASNIVH RVKESLTTRV SKLICAIFLS LLLCLGIITF  
 ILWISLQPHR PRVHIRGFSI SGLSRPDGFE TSHISFKITA HNPQNNGIY YDSMEGVSYY  
 KEKRIGSTKL TNPFYQDPKN TSSIDGALS PAMAVNKDRW MEMERDRNQG KIMFRLKVR  
 MIRFKVYTW HSKSHKMYASC YIEIGWDGML LSATKDKRCP VYFT\*

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## At3g52470

MSKDCGNHGG GKEVVVRKLC AAIIFIVIV LITIFLVWVI LRPTKPRFVL QDATVYAFNL  
 SQPNLLTSNF QVTIASRNP SKIGIYYDRL HVIATYMNQ ITLRTAIPPT YQGHKEVNVW  
 SPFVYGTAVP IAPYNSVALG EEKDRGFVGL MIRADGTVRW KVRTLITGKY HIHVRCAFI  
 40 NLGKAAGVL VGDNAVKYTL ANKCSVNV\*\*

## At5g53730

MSQISITSPK HCAKKGGINI NNRHKKLFFT FSTFFSGLLL IIFLVWLILH PERPEFSLTE  
 ADIYSLNLT STHLLNSSV QLTLSKNPN KKVGIYYDKL LVYAAYRGQQ ITSEASLPPF  
 45 YQSHEEINLL TAFLLQGTLP VAQSFGYQIS RERSTGKIII GMKMDGKLW KIGTWVSGAY  
 RFNVNCLAIV AFGMNMTPP LASLQGTCS TTI\*

## At4g01110

50 MAGETLLKPV LQKPPGYREL HSQPQTPLGS SSSSSSMLRR PPKHAIPAAF YPTKKRQWSR  
 CRVFCVCVCI TVAIVILLI LTVSVFFLYY SPRLPVVRLS SFRVSNFNFS GKGAGDGLSQ  
 LTAEATARLD FRNPNGKLRY YYGNVDVAVS VGEDDFETSL GSTKVKGFE KPGNRTVVIV  
 PIKVKKQQVD DPTVKRLRAD MKSKKLVVKV MAKTKVGLGV GRRKIVTVGV TISCGGVRLO  
 TLDSKMSKCT IKMLKWYVPI QVKCI\*

## 55 At2g35960

MTTKDCGNHG GGGGGGTASR ICGVIIGFII IVLITIFLVW IILQPTKPRF ILQDATVYAF

NLSQPNLLTS NFQITIASRN RNSRIGIYYD RLHVYATYRN QQITLRTAIP PTYQGHKEDN  
VWSPFVYGN VPIAPFNAVA LGDEQNRGFV TLIIRADGRV RWKVGTLITG KYHLHVRCQA  
FINLADKAAG VHVGENAVKY MLINKCSNVN \*

## 5 At3g52460

MPSPPEEETQ PKPDTGPGQN SERDINQPPP PPPQSQPPPP QTQQQTYPPV MGYPGYHQPP  
PPYPNYPNAP YQQYPYAQAP PASYYGSSYP AQONPVYQRP ASSGFVRGIF TGLIVLVVLL  
CISTTITWLW LRPQIPLFSV NNFSVSNFNV TGPVFSQWT ANLTENQNT KLKGYFDRIQ  
GLVYHQNAV G EDEFLATAFF QPVFVETKKS VVIGETLTAG DKEQPKVPSW VVDEMCKERE  
10 TGTVTFSLRM AVWVTFKTDG WAARESGLKV FCGKLKVGFE GISNGAVLL PKPLPCVVYV\*

## At4g09590

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV WIILOPKNPE FILQD'TTVYA  
FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQTILASDL PPTYQRHKED  
15 SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGTLTI GNYHLHVRCQ  
AFINQADKAA GVHVAGENTVK YTLINKCSVN F\*

## At2g35970

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV SILOPKKPE FILQD'TTVYA  
20 FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQTILASDL PPTYQRHKEN  
SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGR VRWKVGTLTI GNYHLHVRCQ  
AFINQADKAA GVHVAGENTVK YTLINKCSVN F\*

## At3g26350

25 MSHHHHHHETN PHFARIPSON PHLKSGGAST SQTSSNQPHI PPIPHPKKSH HKTTQPHPVA  
PPGILIKTRG RHRENPIQEP KHSVIPVPLS PEERLPPRKT QNSSKRPLLL SPEDNQQRQ  
PPPQAPQRNG GYGSTLPPI PKPSPWRTAP TSPHRRGP RLPPPSRETN AMTWSAAFCC  
AIFWVILILG GLIILIVYLV YRPRSPYVDI SAANLNAAYL DMGFLNGDL TILANVTNPS  
KKSSVEFSYV TFELYYYNTL IATQYIEPFK VPKKTSMFAN VHLVSSQVQL QATQSRELQR  
30 QIETGPVLLN LRGMFHARSH IGPLFRYSYK LHTHCSVSLN GPPLGAMRAR RCNTRK\*

## At3g11660

MKDCEHHHGHG RRKLIRRIWF SIIFVLFIIF LTILLIWAII QPSKPRFILQ DATVYAFNVS  
GNPPNLLTSN FQITLSSRNP NNKIGIYYDR LDVYATYRSQ QITFPTSIPP TYQGHKDVDI  
35 WSPFVYGTSTV PIAPFNGVSL DTDKDNQVVL LIIRADGRVR WKVGTFITGK YHLHVKCPAY  
INFGNKANGV IVGDNAVYKT FTTSCSVSV\*\*

## At3g44220

MTEKECEHHH DEDEKMRKRI GALVLGFLAA VLFVVFLVWA ILHPHGPRFV  
40 LQDATIYAFN VSQPNYLTSN LQVTLSSRNP NDKIGIFYDR LDIYASYRNQ  
QVTLATLLPA TYQGHLDVTI WSPFLYGTIV PVAPYFSPAL SQDLTAGMVL  
LNIKIDGWVR WKVGTVVSGR YRLHVNCPAY ITLAGHFSGD GPAVKYQLVQ RCAVDV\*

## At1g08160

45 MVPPNPAHQP ARRTQPQLQP QSQPRAQPLP GRRMNPVLCI IVALVLLGLL VGLAILITYL  
TLRPKRLIYT VEAASVQEFA IGNNDDHINA KFSYVIKSYN PEKHVSRYH SMRISTAHNN  
QSAHKNISP FKQRPKNETR IETQLVSHNV ALSKFNARDL RAEKSKGTIE MEVYITARVS  
YKTWIFRSRR RTLKAVCTPV MINVTSSSLD GFQVLCCKTR L\*\*

## 50 At2g01080

MPPPPSSSRA GLNGDPIAAQ NQQPYRSYS SSSASLKGK CCCLFLLFAF LALLVLAVVL  
IVILAVKPKK PQFDLQQVAV VYMGISNPSA VLDPTTASLS LTIRMLFTAV NPNKVGIRYG  
ESSFTVMYKG MPLGRATVPG FYQDAHSTKN VEATISVDRV NLMQAAHADL VRDASLNDV  
ELTVRGDVGA KIRVMNFDSP GVQVLLPSFL PAFCSLSLA \*

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## At5g06330

- MTSKDCGSHD SHSSCNRKIV IWTISIILL ILVVILLVWA ILQPSKPRFV LQDATVFNFN  
VSGNPPNLLT SNFQFTLSSR NPNDKIGIYY DRLDVYASYR SQQITLPSPM LTTYQGHKEV  
NVWSPPFVGGY SVPVAPYNAF YLDQDHSSGA IMLMLHLDGR VRWKVGSFIT GKYHLHVRCH  
ALINFGSSAA GVIVGKYMLT ETCSVSV\*
- 5 **At5g56050**  
MSKFSPPPQS QPQPPTPPW ETPSSKWYSP IYTPWRTTPR STQSTPTTTP IALTEVIVSK  
SPLSNQKSPA TPKLDSMEAH PLHETMVLLQ LRSTRTNPWI WCGAALCFIF SILLIVFGIA  
TLILYLAVKP RTPVFDISNA KLNTILFESP VYFNGDMLLQ LNFTNPNNKL NVRFENLMVE  
10 LWFADTKIAT QGVLPFSQRN GKTRLEPIRL ISNLVFLPVN HILELRQQT SNRIAYEIRS  
NFRVKAIFGM IHYSYMLHGI CQLQLSSPPA GGLVYRNCTT KRW\*
- At3g20600**  
NDR1  
15 MNQONEDTEG GRNCTCCLS FIFTAGLTSI FLWLSLRADK PKCSIQNFPI PALGKDPNSR  
DNTTLNFMVR CDNPKNKDKGI YYDDVHLNFS TINTTKINSS ALVLVGNVTV PKFYQGHKKK  
AKKWGQVKPL NNQTVLRAVL PNGSAVFRD LKTQVRFKIV FWKTKRYGVE VGADVEVNGD  
GVKAQKKGIK MKKSDSSFPL RSSFPISVLM NLLVFFAIR\*
- 20 **At3g54200**  
MSDFSIPKDD KKEEEKPATA MLPPPKPNAS SMETQSANTG TAKKLRRKRN CKICICFTIL  
LILLIAIVIV ILAFTLFKPK RPTTTIDSVT VDRLOASVNP LLLKVLLNLT LNVDSLKNP  
NRIGFSYDSS SALLNYRGQV IGEAPLPANR IAARKTVPLN ITLTLMDRL LSETQLLSDV  
MAGVIPLNTF VKVTGKVTVL KIFKIKVQSS SSCDLSSISVS DRNVTSQHCK YSTKL\*
- 25 **At3g20590**  
non-race specific disease resistance protein, putative  
MTKIDPEEL GRKCTCFEK FIFTTRLGAL ILWLSLRACK PKCSIQNFPI PALSKNLSSR  
DNTTLNFMVR CDNPKNKDKGI YYDDVHLTFS TINTTTTNS DLVLVANYTV PKFYQGHKKK  
30 AKKWGQVWPL NNQTVLRAVL PNGSAVFRD LKTHVRFKIV FWKTKWYRRI KVGADVEVNG  
DGVKAQKKS KTKKSDSSLP LRSSFPIFVL MNLLVFFAIR \*
- At4g39740**  
MSHVTATSLA RFTKVPKPA SSPIVNTKLT TSGGRTAAFM DLSSFRLTVW  
35 DEDTANDSSG KFPWPRFLFF FLTLKTGGSG LNIKPTISAI AQMMNPMTIT  
EMNNQMRLE QKLLLFPGS LFLRLSTILH YPEGSNRPD PLEHALRRSR  
SLGLDQEEAA KKVIRVGRDS KNDYVNVVEN QAASFLRRCG PSKRIQSVNY  
CKSTRQGHEI PDVKPLFPTG GGTQAPSRSR ARYAVPAILL GFAGFVGFLH  
YNDERRAVPR QOASSNSGCG CGSNTTVKGP IIGGPFTLVS TENKIVTEND  
40 FCGKWVLLYF GYSFSPDVGP EQLKMSKAV DKLAILLNPL TFGCLYLYAE  
FDSRILGLTG TASAMRQMAQ EYRVYFKKVQ EDGEDYLVDT SHNMYLINPK  
MEIVRCFGVE YNPDELSQEL LKEVASVSQ\*
- At1g32270 syntaxin, putative**  
45 MVRSDNVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR  
FEATVYYMNQ RLGAVPMPLE YLGSKNTMLL RALFEGQTLV LLKGNERKKF  
EDDQKTGVYR IDVKLSINFR VMVLHLVTWP MKPVVRCHLK IPLALGSSNS  
TGGHKKMLLI GQLVKDTSAN LREASETDHR RDVAQSKKIA DAKLAKDFEA  
ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS QEQRVLMESR  
50 RQEIIVLLDNE ISLINEARIEA REQGIQEVKH QISEVMEMFK DLAVMVDHQQ  
TIDDIDEKID NLRSAQAQK SHLVKASNTQ GSNSSLLFSC SLLFFFLSG  
DLCRCVCVGS ENPRLNPTRR KAWCEEEDEE QRKKQKKKT MSEKRRREEK  
KVKNPNGFVF CVLGHK\*
- 55 **At1g13050**

MSHHHYETNP HFVQFSLQDQ HQGGPSSSWN SPHHHQIPQA HSVAPPRVKI KTRGRHQTEP  
 PETIHESPS RPLPLRPEEP LPPRHNPNSA RPLQLSPREEQ RPPHRGYGSE PTPWRRAPTR  
 PAYQQGPKRT KPMTLPATIC CAILLIVLIL SGLILLLVYL ANRPRSPYFD ISAATLNTAN  
 LDMGYVLNGD LAVVNFTNP SKKSSVDFSY VMFELYFYNT LIATEHIEPF IVPKGMSMFT  
 5 SFHLVSSQVQ IQMIQSQDLQ LQLGTGPVLL NLRGTFHARS NLGSLMRYSY WLHTQCSISL  
 NTPPAGTMRA RRCNTRK\*

**At5g45320**

MPRLTSRHGT SPFIWCAAI CAIISIVVIV GGIIVFVGYL VIHPRVPIIS  
 10 VADAHLDLFLK YDIVGLQTQ LTIVIRVEND NAKAHALFDE TEFKLSYEGK  
 PIAILKAPEF EVVKEKSMFL PYLVQSYPIP LNPTMMQAVD YAVKKDVITF  
 ELKGGSRTRW RVGPLGSVKF ECNLSCQLRF RPSDHSYIPS PCTSAKH\*

**At3g20610**

MDRDDAWEFV VTIVGSLMTL LYVSFLLALC LWLSTLVHHI PRCSIHYFYI PALNKSIISS  
 15 DNTTLNFMVR LKNINAKQGI YYEDLHLSFS TRINNSSLV ANYTVPRFYQ GHEKKAKKWG  
 QALPFNNQTV IQAVLPNGSA IFRVDLKMV KYKVMWKT KRYKLKASVNL EVNEDGATKV  
 KDKEDGIKMK ISDSSPQRLT FFQVCFSIIC VLMNWLIFLA IR\*

**At4g26490**

MVLTKPATVR FNGLDAEPRK DRVILRQPRS SRTSLWIWCV AVFLAIRPRI PVFDIPNANL  
 20 HTIYFDTPEF FNGDLSMLVN FTNPNKKIEV KFEKLRIELF FENRLIAAQV VQPFLQKKHE  
 TRLEPIRLIS SLVGLPVNHA VELRRQLENN KIEYEIRGT KVAHFGMIH YSYQLHGRCQ  
 LQMTGPPTGI LISRNCTTK \*

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**At5g42860**

MHAKTDEVT SLSASSPTRS PRRPAYFVQS PSRDSHDGEK TATSFHSTPV  
 LTSPMGSPPH SHSSSRFSK INGSKRKGHA GEKQFAMIEE EGLLDDGDRE  
 QEALPRRCYV LAFIVGFSLL FAFFSLILYA AAKPQPKIS VKSITFEQLK  
 30 VQAGQDAGGI GTDMITMNAT LRMLYRNTGT FFGVHVTSS IDLSFSQITI  
 GSGSIKKFYQ SRKSQRTVVV NVLGDKIPLY GSGSTLVPPP PPAPIPKPKK  
 KKGPIVIVEP PAPPAPVPMR LNFTVRSRAY VLGLKVQPKF YKRIVCLINF  
 EHKKLSKHIP ITNNCTVTI \*

**At1g45688**

MHAKTDEVT SLAASSPARS PRRPVYVQS PSRDSHDGEK TATSFHSTPV LSPMGSPPHS  
 35 HSSMGRHSRE SSSSRFSGSL KPGSRKVNPN DGSKRKGHGG EKQWKECAVI EEGLLDDGD  
 RDGGVPRRCY VLAFIVGFFI LFGFFSLILY GAAKPMKPKI TVKSITFETL KIQAGQDAGG  
 VGTDMITMNA TLRMLYRNTG TFFGVHVTST PIDLSFSQIK IGSGSVKKFY QGRKSERTVL  
 40 VHVICEKIPL YGSGSTLLPP APPAPLPKPK KKGAPVPIP DPPAPPAPVP MTLFVVRSR  
 AYVLGKLVQP KFYKKIECDI NFEHKNLNKH IVITKNCTVT TV\*

**At4g26820**

MDDEQNLEVE MNQQLLITVI DTEKVPELRP ISSRSHQESE PANISHWSLL FKLFLAITIM  
 45 GACVAGVTFV ILITPTPTV HVQSMHISFA NNLFPVWSAT FSIKNPNEKL HVTYENPSVW  
 LVHRGKLVST ARADSFQKG GEKNEVIVKR NETKVIDEEA AWEMEDEVAV TGGVVGLDMV  
 FSGRVGFYPG TSALWGEQYM SAVCENVSAK LYNVDDEIYG TNRSVLSFDG RLVCSVRLPK  
 YP\*

50

Plants respond in a variety of ways to pathogens. After a recognition of the pathogen, normally mediated by avr and R genes, the resulting response induces a hypersensitive

- response, that results in inhibition of the pathogen. After the recognition, further processes appear to be non-specific. In addition to the hypersensitive response, a second line of defence, defined as the systemic acquired resistance response
- 5 can be triggered, that renders unaffected parts of the plant resistant to a variety of normally virulent pathogens. Several of the RKS and ELS gene products prove to be key regulators in the regulation of the system acquired resistance response.
- 10 Overexpression of several of the RKS and / or ELS genes in plants, either by constitutive promoters, stage and / or tissue specific promoters, or inducible promoters allows the activation of a systemic acquired resistance response in plants.
- 15 Another application can be provided by the activation of a RKS /ELS specific ligand in (transgenic) plants, thereby activating the receptor complex, that finally results in triggered activation of the systemic acquired resistance response in these plants.
- 20 (ref. Generation of broad-spectrum disease resistance by overexpression of an essential regulatory gene in systemic acquired resistance. H. Cao et al. 1998. Proc. Natl. Acad. Sci. USA 95: 6531-6536). Recent literature shows the functional interaction between RKS10 and BRI-1, another class
- 25 of transmembrane LRR receptor kinases (Cell Vol. 110, 213-222 2002). BAK1=RKS10 as described here, interacts with BRI-1 and modulates brassinosteroid signaling; Cell vol 110, 203-212 2002 BRI1/BAK1 a receptor kinase pair mediating brassinosteroid signaling). Brassinosteroids are known to
- 30 function in a broad range of disease resistance in tobacco and rice (Plant Journal 2003, 887-898). The BRI-1 receptor is involved in the binding of systemin, an 18 amino acid polypeptide, representing the primary signal for the systemic activation of defence genes (PNAS 2002, 9585-9590).
- 35 ELS overexpression phenotypes mimic the effects of inactivation of RKS molecules gene products. Either ELS is competing for ligand binding, or ELS inhibits the interactions

between RKS and BRI-1-like gene products. ELS1 overexpression results in dwarf phenotypes in Arabidopsis and tobacco plants, similar as observed for antisense RKS4 and RKS10, and for knock out plants of RKS0 and RKS4.

- 5 Deregulating expression of ELS and / or RKS genes in plant would modify the broad spectrum disease resistance in such plants. This would explain the observed data that brassinosteroids are involved in disease resistance (Plant Journal 2003, 33 887-898. )

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